U.S. DEPARTMENT OF COMMERCE

Requestor's Name:		Serial Number:		
Date:			Art Unit:	
Search Topic: Please write a detailed statementerms that may have a special mplease attach a copy of the sequence.	eaning. Give examples or re	levent citations, authors,	keywords, etc., if know	arched. Define any n. For sequences,
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Date completed: 3/15  Searcher: 1/5 5 6 6 7  Terminal time: 1/15	90- 308-4292	Search Site  STIC CM-1	Vendor	IG STN
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### Schreißer, David

From:

Yu, Misook

Sent:

Wednesday, August 14, 2002 12:56 PM

To:

Schreiber, David

Subject:

09/499,662

73393

M Serveh notes

David,

Is it possible search

1. (X, 18-30 aa)-SEQ ID NO:2-(X, 14 aa)-SEQ ID NO:3-(X, 32 aa)-SEQ ID NO:4-(X, 11 aa) string and

2. (X, 23aa)-SEQ ID NO:5-(X, 15 aa)-SEQ ID NO:6-(X, 32 aa)-SEQ ID NO:7-(X, 10 aa)?

All the SEQ ID NO are small peptides.

Please compare SEQ ID NO:50, 52, 54, 109, 107, 129, 131, 127 against each other. I would like to know what is the differenenes in the segs. They are all 218 aa antibody light chain.

Please compare SEQ ID NO:89, 117, 143, 145, 147, 15# against each other.

Please search SEQ ID 129, 131, 127, 143, 145, 147, 157. They are all amino acid sequences either 218 or 451 aa.

Please search SEQ ID NO:1 (10aa)

Do I have to get approval from someone for these many seq searches?

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

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Page 1

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 14, 2002, 15:23:12; Search time 53.64 Seconds (Without alignments) 7.218 Million cell updates/sec Run on:

US-09-499-662-1 59 1 RTQNTKCRCK 10 Title: Perfect score: Sequence: BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues

Searched:

105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cript	Q63199 rattus norv	773	5 homo	7	P25446 mus musculu	O00220 homo sapien	mus m	P43489 homo sapien	_	P25118 mus musculu	Q9nii5 mesobuthus	Q9nbg9 mesobuthus	P50329 bradyrhizob	P77700 escherichia	035251 rattus norv	P87387 xenopus lae		P45660 leiurus qui	~		bacil	~	homo	P10643 homo sapien		P13487 leiurus qui	_	P04611 human immun	P52585 orf virus (	$\sim$	P03470 influenza a	S	P06819 influenza a
SUMMARIES	ID	TNR6_RAT	TNR6_PIG	TNR6_HUMAN	TNR6_BOVIN	TNR6_MOUSE	T10A_HUMAN	TNR4_MOUSE	TNR4_HUMAN	WNT2_MOUSE	TR1A_MOUSE	SCK2_MESMA	SCK3_MESMA	NOLA_BRAEL	YAHB_ECOLI	VEGD_RAT	WN2B_XENLA	VEGD_MOUSE	SCK3_LEIQH	WNT2_BRARE	WNT2_HUMAN	YPRB_BACSU	T10B_HUMAN	ORP7_HUMAN	CO7_HUMAN	SCK2_LEIQH	SCKC_LEIQH	TAT_HV1ND	TAT_HV1EL	VEGH_ORFN7	T10C_HUMAN	NRAM_IAWIL	NRAM_IAPUE	NRAM_IAPAR
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de	Query Match Len	100.0	100.0	100.0	93.2	86.4	67.8	66.1	66.1	62.7	62.7	61.0	61.0	61.0	61.0	61.0	61.0	61.0	59.3	59.3	59.3	59.3	59.3	59.3	59.3	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6
	Score	59	59	59	52	51	40	39	39	37	37	36	36	36	36	36	36	36	35	35	32	35	35	35	35	34	34	34	34	34	34	34	34	34
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P52172 drosophila P25509 placobdella	P25510 placobdella P01499 apis mellif Q9nii6 mesobuthus	P55950 callinectes O55038 mus musculu	P12453 human immun P23252 hordeum vul	062802 canis famil P22955 red clover	P38565 xenopus lae
SRP_DROME ORN2_PLAOR	ORN3_PLAOR MCDP_APIME SCK1_MESMA	MT2_CALSI SZ13_MOUSE	TAT_HV2SB CR2_HORVU	IL2A_CANFA COAT_RCNMV	MUB1_XENLA
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# ALIGNMENTS

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InterPro; IPR000488; Death.
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Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
"Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                  Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
D25D583C909D9D09 CRC64;
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                                                         BY SIMILARITY.
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 59; DB 1; Length 324; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                             SUPERFAMILY MEMBER 6.
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TNFR-CYS 2.
TNFR-CYS 3.
PROSITE; PS50017; DEATH_DOMAIN; 1. Apoptosis; Receptor; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                    36835 MW;
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Best Local Similarity 100.
Matches 10; Conservative
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Gaps
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
1-Munor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDINE-1713127;
MEDINE-191309137; PubMed=1713127;
Litch N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I., Sameshima M., Hase A., Seto Y., Nagata S.;
"The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.";
Cell 66:233-243(1991).
         Pfam: PF0053; death; 1.
Pfam: PF0053; death; 1.
Pfam: PF00020; TNFR_c6; 3.
SWART; SW0005; DEATH; 1.
PROSITE; PS0052; TNFR_NGFR_1; 2.
PROSITE; PS50057; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 332 TUMOR NECROSIS FACTOR ECCEPTOR
CHAIN 17 332 TUMOR NECROSIS FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen."; J. Biol. Chem. 267:10709-10715(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335 MEDLINE-92268122; Pubmed-1375228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5B8B03682756BF1B CRC64;
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Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
Krammer P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification and molecular cloning of the APO-1 cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 1; Length 332; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                   SUPERFAMILY MEMBER 6.
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TNFR-CYS 2.
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IPR001368; TNFR_c6.
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Best Local Similarity 100.
Matches 10; Conservative
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TISSUE-Urinary bladder;
                                                                                                                                                                                                                                                                                    175
192
332
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332 AA;
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  InterPro;
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CARBOHYD
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01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-2001 (Rel. 34, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)

323 AA.

BOVIN

P51867;

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

Bovidae; Bovinae; Bos.

SEQUENCE FROM N.A. NCBI\_TaxID=9913;

INFRSF6 OR APT1 OR FAS.

Bos taurus (Bovine).

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                                                Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.; "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain."; Nature 384:638-641(1996).
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM000065; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS000505; TNFR_NGFR_1; 2.
PROSITE; PS500505; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
0139942535111410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR RECEPTOR
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TURR-CYS 1.
TURR-CYS 2.
TURR-CYS 3.
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           MEDLINE-97122332; PubMed-8967952;
                                                                                                                                                                                                                                                                                                                                                 EMBL; BC012479; AAH12479.1; -. PIR; A40036; A40036. PIR; S24543; S24543.
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MIM; 134637; -.
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MEDLINE-9626401; Pubmed-8634151;

A YOO J., Stone R.T., Beattie C.W.;

T Cloning and characterization of the bovine Fas.";

"Cloning and characterization of the bovine Light Receiptor. The Receiptor. CASPARSE 4 CASPARSE 4 TO THE ACTIVATION.

ACTIVE CASPARSE (ASPARTATE-SPECIFIC CYSTEINE PROTECLITIC

CASPAGES (ASPARTATE-SPECIFIC CYSTEINE PROTECLITING

APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE AUTORING APOPTOSIS. PAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INUILARITY).

"INUILARITY CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

"INTILARITY: CONTAINS 3 THER-CYS REPEARS."

"INTILARITY: CONTAINS 1 DEATH DOMAIN.

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                                     Gaps
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100.0%; Score 59; DB 1; Length 335; 100.0%; Pred. No. 0.0013; tive 0; Mismatches 0; Indels
Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                RTQNTKCRCK 10
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121 RTQNTKCRCK 130

RESULT

Gaps ò Score 55; DB 1; Length 323; Pred. No. 0.0065; 1; Mismatches 0; Indels 4D88A90E9E1F4892 CRC64; 1; Mismatches TNFR-CYS 1. TNFR-CYS 2. TNFR-CYS 3 36445 MW; 93.2%; Conservative Query Match Best Local Similarity '-has 9; Conserve 323 AA; 171 171 189 45 81 125 238 REPEAT DOMAIN SEQUENCE REPEAT REPEAT 

PROSITE; PS00652; TNFR\_NGFR\_1; 2.
PROSITE; PS50000; TNFR\_NGFR\_2; 2.
PROSITE; PS50017; DEATH\_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.

InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR\_c6.
Pfam; PF00521; death; 1.
SMART; SM00005; TNFR\_c6; 3.
SMART; SM00005; DEATH; 1.

EMBL; U34794; AAC48546.1; -.

HSSP; P25445; 1DDF.

POTENTIAL.

SIGNAL

CHAIN

TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6.

EXTRACELLULAR (POTENTIAL).

POTENTIAL. CYTOPLASMIC (POTENTIAL)

DOMAIN TRANSMEM DOMAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, NATBARE TO OTHER CYTOSOLIC ADAPTOR PROTBINS.
DISBARSE: DEFECTS IN THERSEF ARE THE CAUGE OF A LYMPHOPROLIFERATION DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAPTOR WOLECULE FADD RECRUITS CASPAGE-8 TO THE ACTIVATED RECRUITS CASPAGE-8 TO THE ACTIVATED SIGNALING COMPLEX FADD RECRUITS CASPAGE-8 TO THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERPORAS CASPAGE-8 PROTEDLYITC ACTIVE CASPAGE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPAGES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING ACTIVE CASPAGE OF DISCOURTED ACTIVE CASPAGE OF THE SUBSEQUENT CASCADE OF ACAPAGES. FAS-MEDIATED APPROFICES MAY HAVE A ROLE IN THE SUBCOURT. IN THE AUTURE T-CELLS, OR BOTH (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
LIVER, LUNG, HEART, AND ADULT OVARY.
                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-mor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-92148151; PubMed-1371136;
Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
Copeland N.G., Jenkins N.A., Nagata S.;
"The CDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.";
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Lymphoproliferation disorder in mice explained by defects in Fas antigen that mediates apoptosis.";
Nature 356:314-317(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-96 FROM N.A.
MEDLINE-93189576; PubMed-7680478;
Adachi M., Watanabe-Fukunaga R., Nagata S.;
"Aberrant transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92195401; PubMed-1372394;
Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993)
                                                                                                                    327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 3 TWFR-CYS REPEATS.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Immunol. 148:1274-1279(1992).
                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                 (CD3);
INFRSF6 OR APTI OR FAS.
                                                                                                                                                                                                                                                                            (Mouse).
                   1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRODUCTION
                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT LPR
                                                                                                                    TNR6_MOUSE
P25446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagata S.;
                                                                                                  TNR6_MOUSE
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EMBL; M83649; AAA37593.1; -.

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 10A precursor (Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor 4) (INF-related apoptosis-inducing ligand receptor 1) (TRAIL
receptor-1) (TRAIL-R1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.; "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway."; Immunity 7:821-830(1997).

-:- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates apoptosis in a caspase-dependent manner. Can trigger the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.,
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0
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Dixit V.M.;
                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 1; Length 327;
Pred. No. 0.033;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> N (IN LPR).
F6BFFC5ACE356EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The receptor for the cytotoxic ligand TRAIL."; Science 276:111-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 AA.
                                                                                                                                                                                                                                                                                                                                                                         TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                               Pfan, PF00531; death; 1.
Pfan, PF00020; TNFR_c6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00622; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
EMBL; S56486; AAB25700.1; JOINED. PTR; A46484; A46540.1; JOINED. PTR; A46484; A46684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98090092; PubMed-943027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Œ.
                                                                                  MGD; MGI:95484; Infrsf6.
InterPro; IPR000488; Death.
InterPro; IPR001368; INFR_C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.4%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
37418 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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                                                                                                                                                                                                                                                                              21
327
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186
327
79
1123
162
306
43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 TONTKCKCK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TQNTKCRCK 10
                                                                                                                                                                                                                                            Apoptosis; Recept
Disease mutation.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T10A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                              FRANSMEM
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REPEAT
REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                               DOMAIN
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T10A_HUMAN
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INFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                         Barclay A.N.;
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CARBOHYD
CONFLICT
SEQUENCE
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TRANSMEM
DOMAIN
REPEAT
REPEAT
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SIGNAL
CHAIN
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
factor kappaB-pathway and can bind the cytoplasmic adapter molecule FADD/MORT1 which engages initiator caspases such as caspase B leading to subsequent activation of effector caspases that execute apoptotic death of the cell.
SUBCELLUAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Widely expressed. High levels are found in spleen, peripheral blood leukocytes, small intestine and thymus, but also in K562 erythroleukemia cells, MCF7 breast carcinoma cells and activated T-cells.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                          PROSITE; PS5001; DEXTH_DOMAIN; 1.
PROSITE; PS50052; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; Apoptosis; Glycoptoteln; Transmembrane; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKED (GLCNAC. . .) (POTENTIAL).
1E85DCDC2C8760F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.8%; Score 40; DB 1; Length 468;
66.7%; Pred. No. 3.9;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
DEATH.
                                                                                                                                                                                                                                                                                                                                                                            SUPERFAMILY MEMBER 10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 AA.
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                               InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50025 MW;
                                                                                                                                                                                                                   EMBL; U90875; AAC51226.1; -. HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor) (OX40 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
211
156
468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| |:||
183 TRNTACOCK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TQNTKCRCK 10
                                                                                                                                                                                                                               HSSP; P19438
MIM; 603611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNR4_MOUSE
P47741;
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                              STRAIN=BALB/C;
MEDLINE-94044756; PubMed-8228223;
Calderhead D.M., Buhlmann J.E., Van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                     "Gene structure and chromosomal localization of the mouse homologue of rat 0X40\ protein.",
                     Craniata, Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TWRR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                                                                                                                                                                                                                                                                                                                               Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 1; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (PO
A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWFR-CYS 1.
TWFR-CYS 2.
TWFR-CYS 3 (INCOMPLETE).
TWFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Immunol. 25:926-930(1995).
-i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-95255413; PubMed-7737295;
                                                                                                                                                                                                                                                 T-B cell interactions.";
J. Immunol. 151:5261-5271(1993).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
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272 AA;
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Matches 6; Conserv
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                                                                                                           SEQUENCE FROM N.A.
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ID TNR4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=95219871; PubMed-7704935;
Baum P.R., Gayle R.B. III., Ramsdell F., Srinivasan S., Sorensen R.A.,
Baum P.R., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
"Identification of OX40 ligand and preliminary characterization of
P43489; Q13663; Ol. Created) (1-NOV-1995 (Rel. 32, Created) (1-NOV-1995 (Rel. 32, Last sequence update) (1-CCT-2001 (Rel. 40, Last annotation update) (1-CCT-2001 (Rel. 40, Last annotation update) (Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen).
                                                                                                                                                                                                                                       MEDINE-94170844; PubMed-7510240;
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
Hummel M., Fonatsch C., Stein H.;
"The human OX40 homolog: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                             its activities on OX40 receptor.";
Circ. Shock 44:30-34(1994).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TWRR-CYS REPERTS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD134 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
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TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (1
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EMBL; S76792; AAB33944.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001368; TNFR_c6.
Pfam; PF000020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
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                                                                                                                                         Homo sapiens (Human)
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215
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                                                                                                                      INFRSF4 OR TXGP1L
                                                                                                                                                                                           NCBI_TaxID=9606;
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MEDLINE-91122634; PubMed-2279700;
MEDLINE-91122634; PubMed-2279700;
Gavin B.J., McMahon J.A., McMahon A.P.;
"Expression of multiple novel Wnt-1/int-1-related genes during fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and adult mouse development.";
Genes Dev. 4:2319-2332(1990).
-!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY
SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE
REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90126394; PubMed-2693041;
MCMahon J.A., McMahon A.P.;
"Nucleotide sequence, chromosomal localization and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL). SEC265FD3815EF1D CRC64;
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                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
WNT-2 protein precursor (IRP protein) (INT-1 related protein).
WNT-2 OR WNT-2 OR IRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.7%; Score 37; DB 1; Length 360; 66.7%; Pred. No. 10; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the mouse int-1-related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental protein; Glycoprotein; Signal. Signal. 1 25 POTENTIAL. 1 25 WWT-2 PROTEIN. CHAIN 26 360 WWT-2 PROTEIN.
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                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development 107:643-650(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 N
40496 MW;
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                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of
                        WNT2_MOUSE
P21552;
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WNT2_MOUSE
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1; Indels

2; Mismatches

Similarity 66.7%; 65.7%; 65.7%; 65.7%;

Query Match Best Local Similarity Matches 6; Conserv

Score 39; DB 1; Length 277; Pred. No. 3.7;

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MEDLINE-93156721; PubMed-8381516;

A Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;

A Rothe J., Bluethmann H., Gentz R.,

"Genomic organization and promoter function of the murine tumor

"Gentz receptor beta gene.";

MOLECOSIS factor receptor beta gene.";

MOLECOSIS factor receptor FOR TWF-ALPHA. THE ADAPTOR MOLECULE FADD

RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING

AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE

PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

-I- SUBUNIT THE BINDING TO THE EXTRACELLIAR DOMAIN OF THREI LEADS

HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO

THERE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

MILLERS THO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

MILLERS THOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-52039815; PubMed-1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
"Molecular cloning and expression of the mouse Inf receptor type b.";
Immunogenetics 34:338-340(1991).
              umor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-R1)
                                                                                                                                                                                                                                                                                               Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                     Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.;
Cloning, expression and cross-linking analysis of the murine p55
tumor necrosis factor receptor.";
Eur. J. Immunol. 21:1649-1656(1991).
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_raxID=10090;
                                                                                                                                                             Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.; "Loning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94245292; PubMed-8188324;
Bebo B.F., Linthicum D.S.;
"Nucleotide sequence of the TNF type I receptor from a mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-KAPPA B SIGNALING (BY SIMILARITY).

-! SUBCELLULAR LOCATION: Type I membrane protein.

-! SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

-! SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91285014; PubMed=1647956;
                                                                                                                                                   MEDLINE=91187885; PubMed=1849278;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-91246168; Pubmed-1645445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endothelioma cell line.";
Immunogenetics 39:450-451(1994).
                                            INFRSF1A OR TNFR1 OR TNFR-1.
                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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the Swiss Institute of Bioinformatics and the EMBL outstation
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BY SIM
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
N-SMASE ACTIVATION DOMAIN (NSD).
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0710C2E8C3C2B6D9 CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                      EMBL, M60468; AAA39751.1; --
EMBL, X59238; CAA40464.1; --
EMBL, X59238; CAA40464.1; --
EMBL, X59238; CAA40922.1; --
EMBL, M7665; CAA40936.1; --
EMBL, M7665; AAA40465.1; --
EMBL, M7665; AAA40465.1; JOINED.
PIR; A38634; GQMST1.
PIR; S19021; S19021.
PIR; S19021; S19021.
HSSP, P19448; IEXT.
MGD; MGI:1314884; Thfrsfla.
InterPro; IPR001368; Death.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00531; death; 1.
Pfam; PF00531; death; 1.
Pfam; PF00531; death; 1.
Pfam; PF00050; TNFR_C6: 4.
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454 AA;
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SCK2_MESMA
ID SCK2_MI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Romi-Lebrum R., Lebrum B., Martin-Eauclaire M.-F., Ishiguro M., Escoubas P., Wu F.Q., Hisada M., Pongs O., Nakajima T.; Purification, characterization, and synthesis of three novel toxins from the Chinese scorpion Buthus martensi, which act on K+ channels."; Biochemistry 36:13473-13482(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM CHANNEL INHIBITORS SUBFAMILY.
                                                                                                                                                                                                                                                                              MEDIINE-20164067; PubMed-10698710;
Dai L., Wu J.J., Gu Y.H., Lan Z.D., Ling M.-H., Chi C.-W.;
"Genomic organization of three novel toxins from the scorpion Buthus martensi Karsch that are active on potassium channels.";
Biochem. J. 346:805-809(2000).
                                             01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
17 Ain BmTX2 precursor (Neurotoxin TX2).
Mesobuthus martensii (Manchurian Scorpion) (Buthus martensii).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20436245; Pubmed=10978761;
Zeng X.-C., Zhu Z.H., Li W.-X., Zhu S.-Y., Peng F., Mao X., Liu H.;
Zeng X.-C., Thouse and genomic organization of a K(+) channel toxin
from the Chinese scorpion Buthus martensii Karsch.";
ToxIcon 39:407-410(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blanc E., Romi-Lebrun R., Bornet O., Nakajima T., Darbon H.; "Solution structure of two new toxins from the venom of the Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scorpion Buthus martensi Karsch blockers of potassium channels.";
Blochemistry 37:12412-12418(1998).
-:- FUNCTION: Potent blocker of both large-conductance calcium-
activated potassium channels (BKCa channels) and voltage-gated
potassium channels (Kv1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom; P0003588; Charybdotxin; 1.
PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
Neurotoxin; Potassium channel inhibitor; Signal; 3D-structure.
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PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 22-58, SYNTHESIS, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF208300; AAF63972.1; -.
EMBL, AF247058; AAK73518.1; -.
PDB), 2BMT; 13-JAN-99.
InterPro; IPR001947; Charybdotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Venom;
MEDLINE=98400946; PubMed=9730813;
                          Created)
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                                                                                                                                                                           Buthoidea; Buthidae; Buthus
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                  01-MAR-2002 (Rel. 41, 01-MAR-2002 (Rel. 41, 01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=34649;
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SIGNAL
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A PARTIES OF THE PROPERTY OF T
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Length 58;

Score 36; DB 1; Pred. No. 3.2;

61.0%; 55.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: Blocks potassium channels.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CHANNEL INHIBITORS SUBFAMILY.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ye J., Li Y., Yan Y., Ji Y.; "Isolation, characterization and cDNA cloning of a novel toxin from the Chinese scorpion Buthus martensi Karsch, which acts on potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                 Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
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Indels
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A1A1A2C415D456A7 CRC64;
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                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Toxin BMTX3 precursor (Neurotoxin TX3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                          59 AA.
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOXIN BMTX3
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SWART; SW00505; Knot1; 1.
PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
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                                                                                                                                                                                          PRT;
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InterPro; IPR003614; Knot1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Ji Y.;
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55.6%;
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5; Conservative
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Pfam; PF00451; toxin_2;
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Matches 5; Conserv
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50 KCQNNQCRC 58
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                                          1 RTQNTKCRC
                                                                                 48 KCMNSKCRC
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P50329;
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                                                                                                                                                                      SCK3_MESMA
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REGULATORS.
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Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
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STRAIN-K12 / MG1655,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rlattner F.R., Plunkett G. III, Sloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                   SOYBEANS.
                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBL_TaxID=29448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
                                                                                                      Dobert R.C., Breil B.T., Triplett E.W.;
"DNA sequence of the common nodulation genes of Bradyrhizoblum
elkanii and their phylogenetic relationship to those of other
nodulating bacteria.";
mol. Plant Microbe Interact. 7:564-572(1994).
-i- FUNCTION: INVOLYDE IN GENOTYPE-SPECIFIC NODULATION OF SOYBE
-i- SUMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00376; mezn, ...
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Nodulation; Nitrogen fixation; DNA-binding.
32 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        219 AA; 24922 MW; 64EA962E8463F029 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical transcriptional regulator yahB.
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                                                                                 STRAIN-USDA 94;
MEDLINE-95036537; Pubmed-7949325;
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000551; HTH_MerR. Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             61.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                           EMBL; U04609; AAA63596.1;
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Matches 5; Conservative
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            Bradyrhizobium elkanii
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                                                                    SEQUENCE FROM N.A.
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P77700;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00126; HTH_1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.0%; Score 36; DB 1; Length 310; 71.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 H-T-H MOTIF (POTENTIAL).
34866 MW; A3EB895E7F69D60C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                    EMBL; AE000138; AAC73419.1; -.
                                                                                                                                                                                                                                                                                                                                                         EMBL, U73857; AAB18042.1; -.
BCOGENG, EG1586; YAHB.
INTERPLO; IPR00197; HTH_FIS.
INTERPO; IPR000847; HTH_LYSR.
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Matches 5; Conserv
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229 NTKCQCQ 235
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Search completed: August 14, 2002, 15:23:12 Job time: 685 sec

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Gaps

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Score 36; DB 1; Length 326; Pred. No. 14; 1; Mismatches 0; Indels

Ouery Match
Best Local Similarity 83.3%;
Matches 5; Conservative

4 NTKCRC 9 ||||:| 235 NTKCKC 240

oy B Appli Appli

Sequence 6, Al Sequence 2, Al Sequence 2, Al Sequence 10, Sequence 11, Sequence 7, Al Sequence 7, Al Sequence 2, Al Sequence 12, A

Sequence

Sequence 11, Sequence Sequence Sequence

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GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YOUNEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: James W. Hellwege
STREET: P.O. BOX 2266 EadS Station
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 59; DB 2; Length 119; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 10; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFLCATION: 435
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILLING DATE: 22-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08219237B Patent No. 5874546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 5167(
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-219-2378-3
      STREET: P.O. BOX CITY: Arlington STATE: Virginia COUNTRY: USA
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        Query Match
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Sequence 14, Appl
                                                                                                                                        August 14, 2002, 15:17:02 ; Search time 82.88 Seconds (without alignments) 2.947 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Compugen Ltd.
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US-09-180-100-9
US-09-180-100-10
US-09-180-100-11
US-09-180-100-12
US-08-180-100-13
US-08-974-022-45
US-08-95-447A-45
US-08-995-447A-45
US-08-995-447A-45
US-08-995-447A-45
US-08-995-447A-45
US-08-995-447A-19
US-08-95-17-238-19
US-08-95-17-238-19
US-08-95-17-238-19
US-08-95-17-238-19
US-08-95-17-238-19
US-08-95-17-238-19
US-08-95-17-238-19
US-08-95-17-238-19
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US-08-409-338-1
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US-09-290-640-2
US-09-006-353A-7
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US-09-180-100-20
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                                                                                                                                                                                                                                                                                                                                                                    231628 seqs, 24425594 residues
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                       GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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59
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Match 1
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Maximum DB
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Patent No. 627098
GENERAL INFORMATION:
APPLICANT: ITOH, Naoto
APPLICANT: TOOH Naoto
APPLICANT: YOURHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILNG DATE: 07-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION NUMBER: U104039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: U191229
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: U19129
FILING DATE: 06-AUG-1989
APPLICATION NUMBER: U190339
FILING APPLICATION NUMBER: U190339
FILING APPLICATION NUMBER: U190339
FILING APPLICATION NUMBER: U190339
ATTONEY/AGENT NUMBER: U190339
ATTONEY/AGENT NUMBER: U190339
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TELEPHONE: 202-628-5197
TELEPAX: 202-737-35.28
INFORMATION FOR SEQ ID NO: 5:
                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STRRET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 100.0
Matches 10; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RTQNTKCRCK 10
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US-08-468-560C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY_AGENT INFORMATION:
NAME: TOWNSEEN'G KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-628 5197
TELEFAX: 202-737-3528
                                                                             Sequence 14, Application US/08477347

Sequence 14, Application US/08477347

Patent No. 622246

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BELEGA, Jacek
APPLICANT: BELETSKY, IGOR
TITLE OF INVENTION: TF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STRRET: 419 Seventh Street, N.W.
CITY: Washington
CITY: Washington
CONNEDED: CONNEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PAROR APPLICATION DATA:
PAPLICATION NUMBER: 08/115,685
FILING DATE:
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 100.
Matches 10; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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                                                       RESULT 2
US-08-477-347-14
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22040-0747

Sequence 5, Application US/08476862
Patent No. 626239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, IGOR
APPLICANT: METT, IGOR
APPLICANT: ENGELMANN, HARTMUT
TITLE OF INVENTION: TNF INHIBITORS

RESULT 3 US-08-476-862-5

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Gaps

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Query Match 100.0%; Score 59; DB 4; Length 143; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 10; Conservative 0; Mismatches 0; Indels
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US-09-180-100-15
Sequence 15, Application US/09180100
Setent No. 6306395
GENERAL INFORMATION:
APPLICANT: NARAMURA, No. 630639510
APPLICANT: NARAMURA, No. 630639510
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 157
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INC. 0305393)
GENERAL INC. 0305391
GENERAL INCORNATION:
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REPERENCE: 1110-207P
CURRENT FILING DAFE: 1998-11-02
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: 1444
    TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
                 FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER PEPLICATION NUMBER: PCT/JP97/01502
SARILER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 193
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US-09-180-100-21
Sequence 21, Application US/09180100
; Patent No. 6306395
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-180-100-10
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                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DAPA:
APPLICATION NUMBER: US/08/468,560C
FILING DAPE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAKATA, Shijekazu
TITLE OF INVERTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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NAME: MORPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09180100 Patent No. 6306395
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APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-9
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76 RTQNTKCRCK 85
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US-09-180-100-10
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Query Match 100.0%; Score 59; DB 3; Length 219; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 10; Conservative 0; Mismatches 0; Indels
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STREET: 1840 Dehavilland Drive
CITE: California
COUNTRY: USA
ZITE: Thousand Oaks
STATE: California
COUNTRY: USA
ZITE: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
FILING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEOUGH 45A-45
Sequence 45, Application US/08795445A
Sequence 45, Application US/08795445A
Fatent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                  ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-022-45
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                                                                                                                               Query Match
100.0%; Score 59; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAKAMURA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-1207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45, Application US/08974022; Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: BOYLE, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TILLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-DEC-1995
GLASSFIECATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09180100 Patent No. 6306395
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APPLICATION NUMBER: 08/577,788
; ORGANISM: Homo sapiens US-09-180-100-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-180-100-23
                                                                                                                                                                                                                                                                                                          105 RTQNTKCRCK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RTQNTKCRCK 10
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ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RTQNTKCRCK 10
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US-09-180-100-23
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US-08-974-022-45
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LENGTH: 159
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100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 121 RTQNTKCRCK 130 g

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/974,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/08795446B
; Sequence 45, Application US/08795446B
; Patent NO. 628803;
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES:
ADDRESSEE: ANGEN INC.
STREET: 1840 Dehavilland Drive
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/577,788
                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/POCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Winter, Robert B.
REPERBUNE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    LENGTH: 219 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMFUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
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MOLECULE TYPE: protein
US-08-974-186-45
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                     APPLICANT: BOyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         US-08-795-447A-45; Sequence 45, Application US/08795447A; Patent No. 6284728; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Amgen Inc.
1840 Dehavilland Drive
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INPORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavill
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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US-09-527-236A-3
Sequence 3, Application US/09527236A
Facent No. 6358508
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Tan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PR375P1
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT APPLICATION NUMBER: 00/00-03-16
PRIOR APPLICATION NUMBER: 00/052,991
PRIOR PILING DATE: 1997-06-11
PRIOR PILING DATE: 1998-06-10
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR PILING DATE: 1999-03-14
PRIOR PILING DATE: 1999-03-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 3
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Ouery Match
100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-3
                                                                                                                        ||||||||||
121 RTQNTKCRCK 130
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121 RTQNTKCRCK 130
                                                                                             1 RTQNTKCRCK 10
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Search completed: August 14, 2002, 15:17:03 Job time: 686 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on:
August 14, 2002, 15:15:34; Search time 230.21 Seconds

(without alignments)
4.825 Million cell updates/sec

Title:
US-09-499-662-1
Sequence:
1 RTONTKCRCK 10
Scoring table:
BLOSUM62DX
Gapop 10.0, Gapext 0.5
Searched:
747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq Database : A\_Geneseq\_032802:\*

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21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Fas epitope recodn	Human Fas epitope,	Human Fas extracel	Human Fas peptide	Human Fas epitope,	Human Fas extracel	Human Fas peptide	Human Fas antigen	Human Fas antigen	Rat Fas receptor.	Human Fas receptor
SUMMARIES			TD .	AAW83030	AAB14740	AAW90890	254W83053	AAB14761	AAW90911	AAY69517	AAW50286	AAW50288	AAB36228	AAB36229
			E I	19	21	21	6	21	21	21	18	18	21	21
		Query	ength I	10	10	10	k	20	20	20	144	159	170	173
	æ	Query	Match 1	100.0	100.0	100.0	198	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	59	59	59	59	59	59	59	59	29	59	29
		Result	No.	н	7	æ	ļ	S	ø	7	89	6	10	11

Fas protein. Unid	Human Fas. Homo s	Fas-delta-TM. Hom	Human Fas soluble	Soluble Fas recept	Human Fas receptor	Human cell surface	Human Fas protein.	Human Fas antigen.		Human Fas antigen.	Fas protein, Mamm	Amino acid encodin	Human Fas receptor	CD-95 (FAS/APO-1)	Human tumour necro	Human Fas antigen	Antigenic peptide	Expression vector	Fas antigen #1. S	Human TNFR1 protei	Plasmid fragment p	Murine Fas. Mus m	Murine Fas antigen		Fas ligand (Fast)	Amino acid sequenc	Expression vector	Fas antigen #2. S	Human colon cancer	A human interphoto	Human interphotore	tvb polypeptide.	Human APORP protei
AAB66978	AAB26982	AAR76238	-AAR99683	AAW98070	AAB50893	AAR28084	AAR78606	AAR99681	AAR92528	AAW50289	AAW49104	AAB19341	AAB36267	AAB01335	AAB50517	AAW50287	AAW60037	AAR78610	AAR92526	AAW64484	AAR78612	AAR41688	AAR78611	AAR92530	AAW86241	AAB19344	AAR78613	AAR92527	AAB53420	AAY93336	AAY57089	AAW41360	AAW93577
22	21	16	7	20	22	13	16	17	17	18	19	21	21	21	22	18	19	16	17	19	16	14	16	17	20	21	16	17	21	21	21	19	20
219	281	314	314	314	331	335	335	335	335	332	332	335	335	335	335	376	376	909	009	699	169	327	327	327	327	327	216	592	237	771	771	368	410
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	186.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	74.6	69.5	69.5	67.8	67.8
59	29	29	29	59	59	29	29	29	29	29	5	29	59	59	59	59	59	59	59	59	51	51	51	51	51	51	21	51	44	41	41	40	40
12	13	14	15	£	17	18	19	20	21	22	23	24	25	36	27	28	29	30	31	38	F	34	35		. 37	38	39	40	41	42	43	44	45

## ALIGNMENTS

scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy. Fas; epitope; HFE7A; monoclonal antibody; humanised antibody; human; apoptosis; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus, graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; Fas epitope recognised by MAb HFE7A. AAW83030 standard; Peptide; 10 AA. 97JP-0276064. 97JP-0082953. 97JP-0169088. 98AU-0059701. (first entry) 08-OCT-1997; 01-APR-1997; 25-JUN-1997; 15-MAR-1999 Homo sapiens 30-MAR-1998; AU9859701-A. 08-OCT-1998. AAW83030; AAW83030  ~

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29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serizawa N,
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                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Fas epitope, anti-Fas antibody, murine monoclonal antibody HFE7A,
FERM-BP-5828, humanised antibody, complementarity determining region,
CDR; Fas ligand, apoptosis modulator, programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                      used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                 This peptide represents the human Fas epitope recognised by novel murine anti-human Fas monoclonal antibody HFE7A. It was identified by ELISA and competitive assays using peptides (see AAW8043-63) from the extracellular domain of Fas. The epitope is conserved between mouse and human Fas. The invention provides humanised HFE7A antibodies (see AAW8031-37) produced by CDR graftling. These antibodies bind to the Fas epitope. They are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas autofummune disease (systemic lupus erythematosus, Hashimoto's advector and also to treat such diseases.
                                                                                          New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                                                                                                                                                              disease, graft versus host disease, Siogrem syndrome, permittions anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiphe sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allerquies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 59; DB 19; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0033; Matches 10; Conservative 0; Mismatches 0; Indels
                          Jun O, Kimihisa I;
Tohru T;
                         Akio S, Hideyuki H, Hiroko Y, Ju
Masahiko O, Nobufusa S, Shin Y,
                                                                                                                                                           Claim 20; Page 184; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB14740 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Fas epitope, SEQ ID NO:1.
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(SANY ) SANKYO CO LTD
                                                                WPI; 1998-543440/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RTQNTKCRCK 10
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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine arti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AABI4740 and AABI4751-BI4771
                                                                                                                                                  Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 59; DB 21; Length 10; 100.0%; Pred. No. 0.0033; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                        Claim 19; Page 31; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW90890 standard; peptide; 10 AA.
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98JP-0276882.
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Matches 10; Conservative
(SANY ) SANKYO CO LTD.
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                                                                           WPI; 2000-485645/43.
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AAB14761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                into Inventor describes a novel numarized anti-ras antibody. Times a now describes a novel numarized anti-ras antibody. The molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by bindibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-amemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunoadulatory, dermatological, immunosuppressive, thyromimetic, antidiabetic, antidiffertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's moultiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, and transplant rejection. (I) selectively induce it in abnormal cells but selectively induce it in abnormal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the mative ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                         New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human, apoptosis; HFETA, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; sjoren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; attornomenia prepura; insulin-dependent diabetes; allergy; attory; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitope; HFE7A; monoclonal antibody; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 59; DB 21; Length 10; 100.0%; Pred. No. 0.0033; ive 0; Mismatches 0; Indels
                                                                                                       Example reference 6; Page 97; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW83053 standard; Peptide; 20 AA.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
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FERM-BP-5828; humanised antibody; complementarity determining region; CDR; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Fas epitope; anti-Fas antibody; murine monoclonal antibody HFE7A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic peptides P1-P15 (see AAW83043-57) are partial sequences of amino acids 1-157 of the extracellular domain of human Fas, with between 9 and 11 amino acid residues overlapping one another. P16 (see AAW83058) is a negative control having no homology with human Fas. P1-P16 were used in an ELISA, which demonstrated that novel murine anti-human Fas monoclonal antibody HFE7A specifically binds an amino acid sequence contained in P11. The epitope (see AAW83030) was subsequently identified. The invention provides humanised HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                        Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 59; DB 19; 100.0%; Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference Example 6; Page 87; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                             97JP-0276064.
97JP-0082953.
97JP-0169088.
                                                                                                                              98AU-0059701.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                 30-MAR-1998;
                                                                                                                                                                                                                                01-APR-1997;
25-JUN-1997;
                                                                                                                                                                                                    08-OCT-1997;
AU9859701-A.
                                                                  08-0CT-1998
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98JP-0276882.

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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthitis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                      The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14740 and AAB14751-B14771
                                                                                                                               Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 59; DB 21; Length 20; I Similarity 100.0%; Pred. No. 0.0061; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Fas extracellular domain antigenic peptide #11.
                                                                                                                                                                                 Example 6; Page 30; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW90911 standard; peptide; 20 AA.
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                           99JP-0278301.
                                                  98JP-0276883
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                                                                             (SANY ) SANKYO CO LTD.
                                                                                                     WPI; 2000-485645/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                           30-SEP-1999;
                                                  30-SEP-1998;
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20-JUN-2000
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This invention describes a nove numarized anti-ras antibody—like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ignand system, by binding to Fas on the cell surface, and prevents cappetosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, cantin-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiartheomatic, nephrotropic, antidiffertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent disease associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's Syndrome, pernicious or hypoplastic anemia, Addison's disease, relardermactoid arthritis, graft versus host disease, scleroderma, Goodpasture syndrome, Conn's disease, autoinmune hemolytic anemia, sterility, mysathenia gravis, altiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral cells. They bind to both human and murine Fas, so can be evaluated in thinbit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antisease, and have reduced risk of the native ligand, do not induce liver disease, and have reduced risk of human pare particular domain derived antigenic peptide described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                         New humanized anti-Fas antibody, useful for treating or preventing e.g.' inflammatory or autoimmune disease, induces apoptosis selectively in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel humanized anti-Fas antibody-like
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modulator; apoptosis; proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
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                                                                                          Takahashi T;
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                                                                                          Nakahara K, Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example reference 6; Page 110; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                        cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY69517 standard; peptide; 20 AA.
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                                                                                          Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
(SANY ) SANKYO CO LTD.
                                                                                                                                                                                    WPI; 2000-258930/23
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                                                                                          Serizawa N,
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Chiodi F;

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Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
of viral and other diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                   contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 18; Length 1 100.0%; Pred. No. 0.035; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a Fas antigen derivative, which
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17..159
/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW50288 standard; Protein; 159 AA.
                                                                                                                          (MOCH ) MOCHIDA PHARM CO LTD. -
(OSAB-) OSAKA BIOSCIENCE INST.
                                                                               96JP-0135760.
                                        97WO-JP01502.
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                                                                                                                                                                                    Nagata S, Nakamura N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues are deleted)
                                                                                                                                                                                                                           WPI; 1997-558981/51.
N-PSDB; AAV07003.
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                                        01-MAY-1997;
                                                                                 02-MAY-1996;
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  13-NOV-1997
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Matches
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                                                                                                                                                                                                                                                                                                                   Sequences AAV69514-Y69521 represent peptide fragments of the Fas protein (also known as APO-1 or CD95). Fas is a type I cellular receptor which transduces an apoptotic signal on binding of its ligand, Fas ligand (Fas-Ball). Fas autoantibodies have been isolated from the serum of healthy blood donors - these may represent an additional mode of regulation of Fas-mediated signals in vivo. The Fas peptides may be used to modulate apoptosis via blocking autoantibody binding to Fas, thereby reducing or increasing Fast binding, which results in inhibition or stimulation of apoptosis. Fp5 (AAY69514) is thus able to induce apoptosis while Fp11 (AAY69515) and Fp9 (AAX69516) comprise amino acids which are important for binding of Fas to Fast. The Fas peptides can be used to obtain the used in assay methods to obtain candidate modulators of Fas-mediated apoptosis. The candidate modulator may also modulators of Fas-mediated apoptosis. The candidate modulator may also modulators of Fas-mediated apoptosis. The resulting proliferation The peptides, mixtures of peptides, nucleic acids or antibodies are useful for methods of treating proliferative disorders. The disorders that may be prevented or treating proliferative disorders. The perinasis, type I diabetes, multiple sclerosis, liver cirrhosis and HIV
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                                                                                                                                                                                                            Fas peptide fragments useful for the treatment of proliferative disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 21; Length 20; llarity 100.0%; Pred. No. 0.0061; Conservative 0; Mismatches 0; Indels
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/label= sig_peptide
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/label= mat_peptide
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                                                                                                  (KARO-) KAROLINSKA INNOVATIONS AB.
                                                                                                                                                                                                                                                                                       Claim 3; Page 57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fas antigen derivative.
                                        98GB-0013194.
99WO-EP04105.
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                                                                                                                                                                                WPI; 2000-106082/09.
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                                        18-JUN-1998;
12-MAR-1999;
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15-JUN-1999;
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Sequence

Query Match Local

Best Loc Matches

AAW50286;

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AAW50286 RESULT

Peptide Peptide

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Gaps

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Length 144;

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173 AA;
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                    factor receptor
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                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                     WO200063369-A2.
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                       Sequence
                                                                                                                                                                                                                                                                   AAB36229;
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Matches
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                                                                                                                                                                                                                                                                                               Gaps
                                                                                Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
of viral and other diseases
                                                                                                                                      The present sequence encodes a Fas antigen derivative/IgG1 hinge fusion, which contains a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted).

The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding bMA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases with as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1; accelerated graft arteriosclerosis; vascular occlusive disease.
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                                                                                                                                                                                                                                                                              Length 159;
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                                                                                                                                                                                                                                                                            Score 59; DB 18;
Pred. No. 0.038;
                                                                                                                                                                                                                                                                                              Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(UYJO ) UNIV JOHNS HOPKINS.
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                                                                                                                     Disclosure; Fig 5; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                            AAB36228 standard; Protein; 170 AA.
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                                                                                                                                                                                                                                                                            100.0%;
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         MOCHIDA PHARM CO LTD.
OSAKA BIOSCIENCE INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                              10; Conservative
                                     Nakamura N;
                                                                                                                                                                                                                             virus-infected cells
                                                     WPI; 1997-558981/51
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Best Local Similarity
                                                                                                                                                                                                                                                                                                               1 RIQNTKCRCK 10
                                                                                                                                                                                                                                                 159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Fas receptor.
                                                               N-PSDB; AAV07005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC66557
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10-MAY-1999;
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                                    Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                               AAB36228;
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                  (OSAB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of gene therapy which involves the use of RasR or FGFR-1 coding sequences to treat vascular diseases. The invention also provides vectors for use in this method. The treatable diseases include vascular occlusive diseases associated with cell proliferation, such as accelerated graft arterlosclerosis and other forms of stenosis.
   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
proliferation, comprises transferring, to cells or progenitors, the sequence encoding Fas antigen or receptor, or the fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1; accelerated graft arteriosclerosis; vascular occlusive disease.
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larity 100.0%; Pred. No. 0.04;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanfilippo A;
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(UYJO ) UNIV JOHNS HOPKINS.
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                                                                                                                                              Disclosure; Page 33-34; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36229 standard; Protein; 173 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000; 2000WO-EP03532.
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Best Local Similarity
Matches 10; Conserv
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The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAFS7836-AAFS7838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGP)-10 modulators and/or platelet activating factor (PRF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                        Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condution; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischemnia; parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock The present sequence was used in a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukln and tumor necrosis factor alpha -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLB) a graft-versus-host disease (GVHD). Other diseases that can be treated include acute pencreatitis. Alzheimer's disease, anorexia.
                                           Gaps
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100.0%; Score 59; DB 21; Length 173; 100.0%; Pred. No. 0.041; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                    AAB66978 standard; Protein; 219 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-2000; 2000WO-US18667.
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                                                                                                                                                                                                                                                                                                (first entry)
                                     10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-103031/11.
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                                                                                                                   121 rtgntkcrck 130
Query Match
Best Local Similarity
                                                                              1 RTONTKCRCK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                       Fas protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is Fas, a member of the tumour necrosis factor receptor family. A novel human tumour necrosis factor receptor, designated TR9, has been isolated. The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for treating, preventing or diagnosing common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
                                                                                                                                                                                                                                                                                                                                            Human; Fas; tumour necrosis factor; TR9 receptor; immunosuppressive; antidiamatory; cardiant; antiasthmatic; antidiabetic; antiallergic; antiathritic; antirheumatic; anti-HTV; anticonvulsant; cytostatic; neuroprotective; gene therapy; Death Domain Containing Receptor 6; common variable immunodeficiency; X-11nked agammaglobulinaemia; severe combined immunodeficiency; Wiskott-Addrich syndrome; autoinmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data.
                                     Gaps
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 Length 219;
                                    0; Indels
100.0%; Score 59; DB 22;
100.0%; Pred. No. 0.051;
ive 0; Mismatches 0;
                                                                                                                                                                                                     AAB26982 standard; Protein; 281 AA
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Best Local Similarity 100.
Matches 10; Conservative
                                    Conservative
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 Ouery Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                              Human Fas.
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A natural, soluble Fas antigen variant (AAR99682), designated Fas dell, and other Fas variants (AAR99683-85) are derived by alternative splicing of Fas gene transcripts. A cDNA clone (AAT34527) coding for the variant was obtd. from human peripheral blood mononclear cells. The Fas dell variant lacks the transmembrane domain of insoluble Fas antigen (AAR99681). Recombinant dell variant, or fragments of it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells. Detection of increased levels of soluble forms of Fas antigen can be used to diagnose autoimmune diseases, esp. systemic lupus erythematosus and angioimmunoblastic lymphadenopathy.
Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE; angioimmunoblastic lymphadenopathy; AILD.
                                                                                                                                                                                                                                                                           "preferred peptide from breakpoint region"
                                                                                                                                                                                                                                                                                                   "preferred peptide from breakpoint region"
                                                                                                                                                                                                                                       /note= "preferred peptide from breakpoint region
  (claim 4, page 132)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natural, soluble form of Fas antigen secreted by human cells is result of alternative mRNA processing – used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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Pred. No. 0.07;
Mismatches 0; Indels
                                                                                                                             /note-
17..168
/label=Extracellular_domain
/note- "the 5 C-terminal residues of the
Fas antigen extracellular domain
deleted in Fas dell"
                                                                                            17.23.4
| 7.Tabel = Mat_protein
| // Mare = "soluble Fas dell antigen"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 114-16; 152pp; English.
                                                                           1..16
/label= Sig_peptide
                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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161..171
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Best Local Similarity 100.
Matches 10; Conservative
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N-PSDB; AAT34527.
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                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                               WO9620206-A1.
                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCF product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. The insert sequence of pBluescript-Fas-delta-TM encoded the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 314;
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(. 0.07;
                                                                                                                                                                          Fas-delta-TM; transmembrane deletion; apoptosis; antibody; adoptive immunotherapy; transgenic animal.
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                                                                                                                                                                                                                                                    1..16
/label= Sig_peptide
                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   Shapiro JP;
                                                                       AAR76238 standard; Protein; 314
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                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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           121 rtgntkcrck 130
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N-PSDB; AAQ93879.
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Gaps

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

August 14, 2002, 15:18:58 ; Search time 108.64 Seconds (without alignments) 8.845 Million cell updates/sec Run on:

US-09-499-662-1 59

Perfect score: Title:

1 RTONTKCRCK 10 Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
: pir4:\*.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	137383	JC2395	A40036	A46484	148700	137552	150610	B36470	GQMST1	T09052	D90674	G85524	F81938	D64758	T23462	S00834	C69941	A27340	A60963	B60963	TNLJND	T28303	D49530	S51770	S48186	r18066	C69255	S20711	NMIV3
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34 34	34 34	34 34	34	9 6	33	33	33	33	33	33	33
30 31	32 33	34 35	36	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C; Accession: 137383
B; Cascino, I:; Flucci, G:; Papoff, G:; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A; Fitle: Three functional soluble forms of the human apoptosis-inducing Fas molecule A; Reference number: 137383; MUID:95181785
A; Reference number: 137383
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-314 < RES>
A; Cross-references: EMBL:247993; NID:9728578; PIDN:CAA88031.1; PID:9695539
FAS soluble protein - human
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Gaps ; Ouery Match 100.0%; Score 59; DB 2; Length 314; Best Local Similarity 100.0%; Pred. No. 0.0073; Matches 10; Conservative 0; Mismatches 0; Indels

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121 RTQNTKCRCK 130 1 RTQNTKCRCK 10 ŏ

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Fas antigen precursor - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999
C;Accession: JC2395; PC2345
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat 1
A;Reference number: JC2395; MUID:94128114

A;Molecule type: mRNA A;Residues: 1-324 <KIM> A;Cross-references: DDBJ:D26112; NID:9468486; PIDN:BAA05108.1; PID:d1005650; PID:9468

A; Experimental source: thymus A; Accession: PC2246

A;Molecule type: mRNA A;Residues: 1-62, 'RFT' <KI2> A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468 A;Experimental source: liver C;Genetics:

A;Introns: 62/1 C;Superfamily: NGF receptor repeat homology C;Keywords: transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG>F;22-324/Product: Fas antigen #status predicted <MAT>

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Note: Sequence extracted from NCBI billine
A; Note: NCBI billine
A; NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anolecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Residues: 1-96 <ADA>
A:Residues: 1-96 <ADA>
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Cross-references: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268
C;Superfamily: NGF receptor repeat homology
C;Reywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG6>
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N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: 148700; I48334; S34377
S;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A;Reference number: 148700; MUID:94044750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and chromosomal localization of the mouse homologue of rat OX
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A; Molecule type: mRNA
A; Residues: 1-272 < RES.
A; Residues: 1-272 < RES.
A; Cross-references: ERBL: 221674; NID: 9312827; PIDN: CAA79772.1; PID: 9312828
A; Cross-references: ERBL: 22674; NID: 9312828
B; Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A; Title: Gene structure and chromosomal localization of the mouse homologue of
    C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46484; A47254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:9732818; PIDN:CAA59476.1; PID:9732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 16;
2; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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ilarity 66.78;
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Local 8; Conserve
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Best Local Similarity
Matches 6; Conserv
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C; Species: Homo sapiens (man)
C; Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C; Accession: A40036; S24543; A38142
R; Itch, N; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991
A; Title: The polyPeptide encoded by the cDNA for human cell surface antigen Fas can medi A; Reference number: A40036; MUID:91309137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X63717; NID:928741; PID:928742
R;Ochm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member A;Reference number: A38142; MUID:92268122
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A;Molecule type: mRNA
A;Residues: 1-335 <ITO>
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
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A; Experimental Source: SW64, cells
A; Note: sequence extracted from NCBI backbone (NCBIP:103810)
A; Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis-mediating membrane-associated polypeptide Fas - mouse C;Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis-mediating surface antigen Fas precursor - human N, Alternate names: surface antigen APO-1
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                         Query Match 100.0%; Score 59; DB 2; L
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 0;
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A;Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                              117 RTQNTKCRCK 126
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Best Local Similarity
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DB 44;
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A; Residues: 1-360 <MCM>
C; Superfamily: int-1 transforming protein
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                           62.78;
                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-454 < LEW>
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A; Residues: 1-454 <GO2>
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A; Residues: 1-454 <BAR>
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319 TRMTKCECK 327
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A; Accession: B36470
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R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell surface glycoprotein CD8 alpha chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 150610; 833350
R;Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davlson, J. Immunol. 154, 4485-4494, 1995
A;Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha
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C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 15-Jun-1996
C;Accession: B36470; A43558
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult in A;Reference number: A36470; MUID:91122634
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
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A.Raccession: 150610
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-235 <TRE>
A.Cross-references: EMBL:222726; NID:9488149; PIDN:CAA80421.1; PID:9297781
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Steporfas: 91ycoprotein
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Pred. No. 16;
2; Mismatches 1; Indels
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Pred. No. 32;
3; Mismatches 2; Indels
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A;Residues: 1-277 <RES>
A;Cross-references: EMEL:X75962; NID:g472957; PIDN:CAA535;
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                      A;Reference number: 137552; MUID:94170844
A;Accession: 137552
A;Status: preliminary; translated from GB/EMBL/DDBJ
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N;Alternate names: int-1 related protein
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66.7%;
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50.0%;
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Matches 6; Conservative
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208 KTRRRCRCK 217
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Best Local Similarity
Matches 5; Conserv
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98 TQDTVCRCR 106
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                   TONTKCRCK 10
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B36470
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N.Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I55452; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A;Reference number: A38634; MUID:91187885
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R;Godwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168
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R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Fel
Eur. J. Imminol. 21, 1649-1656, 1991
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A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel A;Reference number: 154532; MUID:94245292
A;Accession: 154532
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRNA
A;Residues: 1-360 <GAV>
                                                                                                                                R;McMahon, J.A.; McMahon, A.P.
Development 107, 643-650, 1989
A;Title: Nucleotide sequence, chromosomal localization and developmental expression
A;Reference number: A43558; MUID:90126394
A;Recession: A43558
A;Status: preliminary; not compared with conceptual translation
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A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.08;
71.48;
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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5 NTKCQCQ 11
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                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393, 'G', 395-454 <RE2>
A;Cross-references: GB:M76656; NID:9202100; PIDN:AAA40465.1; PID:9202102
C;Comment: This protein is one of two distantly related receptors for both INF-alpha (ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09052
R;Habuchi, T.: Luscombe, M.; Elder, P.A.; Knowles, M.A.
Geomatics 48, 277-288, 1998
A;Title: Structure and methylation-based silencing of a gene (DBCCRI) within a candidate A;Reference number: 216537; MUID:98207242
A;Accession: T09052
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                                                                                                                                                                                                                                                                                                          A; Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C; Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C; Superfamily: tumor necrosis factor receptor dy? opportein; receptor; transmembrane protein
F; 1-29/Domain: signal sequence #status predicted <SIGS
F; 30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F; 30-212/Domain: extracellular #status predicted <EXT>
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor
A;Reference number: 157826; MUID:93156721
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Ksesidues: 1-761 cHABD.
A;Cross-references: EMBL:AF027734; NID:g3041876; PIDN:AAC39691.1; PID:g3041877
A;Experimental source: tissue type: brain; developmental stage: fetal and infant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;44-82/Domain: NGF receptor repeat homology <NG1>F;84-126/Domain: NGF receptor repeat homology <NG2>
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Pred. No. 80;
3; Mismatches
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A;Note: IB3089A
C;Superfamily: human hypothetical protein DBCCR1
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Similarity 75.0%;
6; Conservative
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illarity 62.5%;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 5; Conserv
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A;Gene: TNFR-2
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Upporhetical protein 20404 [imported] - Escherichia coli (strain 0157:H7, substrain E Upporhetical protein 20404 [imported] - Escherichia coli (species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli (c;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85524

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001

A;Ritle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Recension: G85524

A;Status: prelliminary

A;Recension: G85524

A;Status: prelliminary

A;Residues: 1-86 csTO>

A;Cross-references: GB:AE005174; NID:g12513132; PIDN:AAG54659.1; GSPDB:GN00145; UWGP: A;Equen: minental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: 20404
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A Modecule type: DNA
A Modecule type: DNA
A Mesidues: 1-86 < HAY>
A Cross-references: GB:BA000007; PIDN:BAB33787.1; PID:g13359821; GSPDB:GN00154
A Experimental source: strain 0157:H7, substrain RIMD 0509952
A Genetics:
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Pred. No. 21;
2; Mismatches
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Pred. No. 21;
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2; Indels
                2; Mismatches
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ne: 686 sec
                5; Conservative
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                Matches
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Job time:
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C; Species: Diodina coli
C; Species: Diodina coli
R; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
R; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichian coli K-12.
A; Reference number: A64720; MUID:97426617
A; Reference number: A64720; MUID:97426617
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-310 cBhAT>
A; Cross-references: GB:AE000138; GB:U00096; NID:91786501; PIDN:AAC73419.1; PID:91786508;
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
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A;Cross-references: EMBL:268316; PIDN:CAA92679.1; GSPDB:GN00022; CESP:K08E4.4
A;Experimental source: clone K08E4
C;Genetics:
C; Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein F;1-21/Domain: signal sequence #status predicted <SIG> F;22-163/Product: cytochrome c552 #status predicted <MAT> F;28-109/Domain: cytochrome c6 homology cXck> R;28-109/Domain: cytochrome c6 homology cXck> F;38,41/Binding site: heme (Cys) (covalent) #status predicted F;42,92/Binding site: heme iron (His, Met) (axial ligands) #status predicted
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T23462
R;Percy, C.
Submitted to the EMBL Data Library, December 1995
A;Reference number: Z19744
A;Reference number: Z19744
A;Reference number: T23462
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Spleanie Type: DNA
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Pred. No. 35;
2; Mismatches 2; Indels
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Pred. No. 58;
2; Mismatches 0; Indels
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55.6%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
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229 NTKCQCQ 235
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A;Map position: 4
A;Introns: 45/3
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09167 tupala herp
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094784 vaccinia vi
0911r5 vaccinia vi
091829 plasmodium
07382 brachydanio
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corpus luteum.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104034; AAD20221.1; ...
InterPro: 1PR001368; TNFR_c6.
InterPro: 1PR001368; TNFR_c6.
SMART; SM00208; TNFR; 2.
PROSITE; PS50050; TNFR, 1; UNKNOWN_1.
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16644 MW; 7DEC76EC40A6BA4F CRC64;
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100.0%; Pred. No. 0.00026;
ive 0; Mismatches 0;
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Q73682
Q9LE55
Q9LE55
Q9UGG
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09JJL6
09QZM4
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PRELIMINARY;
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Q9tsn4 macaca fasc
Q9gx36 macaca assa
Q9bdn cercocebus
Q9bdn macaca neme
Q9bdp macaca mula
Q9d140 macaca mula
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homo sapien
                                                                                August 14, 2002, 15:22:14; Search time 187.61 Seconds (without alignments) 9.221 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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sp_unclassified:*
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sp_rodent:*
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Minimum DB : Maximum DB :

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Perfect score:

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Sequence:

Scoring table:

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Length 314;

RESULT **09GK28** 

SOUR PRESENTATION OF THE PROPERTY OF THE PROPE

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Aotus trivirgatus (Night monkey) (Douroucouli).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).

Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
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Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 59; DB 6; Length 327; 100.0%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5CFEE844B2BE387A CRC64;
                                   83F8FAC62DB8B457 CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN CD95.
                                                                                   100.0%; Score 59; DB 4; 1
100.0%; Pred. No. 0.00049;
iive 0; Mismatches 0;
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Pfant, PPO0531; death; 1.
Pfant, PP00020; TNFR_C6; 3.
SMART; SM00006; DEATH; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50062; TNFR_MSFR_1; 1.
SEQUENCE 327 AA; 36928 WW; 5CFEE
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PSO0652; TNFR_NGFR_1; 1.
PS50050; TNFR_NGFR_2; 2.
314 AA; 35386 MW; 83
                                                                                                                                                                                                                                                                                                                   01-MAY 1999 (TrEMBLrel. 10, 01-MAY 1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17, FAS PROTEIN.
                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                   314 AA;
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SEQUENCE FROM N.A.
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SEQUENCE
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MEDLINE=95181785; PubMed=7533181;
MEDLINE=95181785; PubMed=7533181;
MEDLINE=95181785; PubMed=7533181;

"Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing.";

J. Immunol. 154:2706-2713(1995).

EMBL: 247993; CAA88031.1; --
HSSP; P25445; IDDF.
                                                                                                                                                                                           Macaca arctoides (Stump-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 310;
                                                                                                                                                                                                                                                                                                               Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.; "Cloning of fas gene in stump-tailed monkey."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF332357; AAG49394.1; HSSP; P25445; IDDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH; 1.
PROSITE; PS50052; TNFR_NFR_1; 1.
PROSITE; PS50052; TNFR_NFR_1; 1.
PROSITE; PS50050; TNFR_NFR_1; 1.
PROSITE; PS50050; TNFR_NFR_1; 1.
SROUENCE 310 AA; 34806 MW; C5C79BFIF804A419 CRC64;
                                                             09GK28 PRELIMINARY; PRT; 310 AA. 09GK28: 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PAS ANTIGEN APO-1/CD95.
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Last annotation update)
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100.0%; Pred. No. 0.00048;
Live 0; Mismatches 0;
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InterPro; IPR001368; TNFR_c6.
Pfam; PF000531; death; 1.
Pfam; PF00050; TNFR_c6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
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Q14293;
Q1-NOV-1996 (TrEMBLrel. 01, Cr
Q1-NOV-1996 (TrEMBLrel. 01, La
Q1-DEC-2001 (TrEMBLrel. 19, La
FAS SOLUBLE PROTEIN.
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Best Local Similarity 100.
Matches 10; Conservative
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NCBI_TaxID=9540;
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RESULT 014293

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Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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  PRELIMINARY;
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  Q9GK36
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WEDLINE-20237686; PubMed-10773350;

WARLYAMA Y., Terao K., Inoue-Murayama M.;

WARLYAMA Y., Terao K., Inoue-Murayama M.;

WINTERIAMA Y., TERAO K., Inoue-Murayama M.;

WINTERIAMA Y., TERAO K., Inoue-Murayama M.;

WARDIAL IMMUNOI. 61:474-485(2000).

REMBL, AB031420; BAA83551.1; -.

REMBL, AB031420; BAA83551.1; -.

REMBL, PRO0148; Death.

REAP FEAR PRO01368; TERE_C6.

DR FEAR, PRO01020; TERE_C6; 2.

DR SWART; SW00005; DEATH; 1.

DR SWART; SW00005; TERE_NOMAIN; 1.

DR PROSITE; PS50017; DEATH, DOMAIN; 1.

DR PROSITE; PS50017; DEATH, DOMAIN; 1.

DR PROSITE; PS50050; TNFR_NGFR_1; 1.
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           T. "Cloning, sequencing, and homology analysis of nonhuman primate
T. "Cloning, sequencing, and homology analysis of nonhuman primate
T. "Eas/Fas-ligand and co-stimulatory molecules.";
Immunogenetics 53:315-328(2001).
Immunogenetics 53:315-328(2001).
Interpro; IPR000488; Death.
Interpro; IPR000488; Death.
Interpro; IPR000488; Death.
Interpro; IPR000488; Death.
IN PROSTIC: PS50017; DEATH.DOMAIN; 1.
R. SMART; SM00005; DEATH.DOMAIN; 1.
R. PROSTIE: PS50017; DEATH.DOMAIN; 1.
R. PROSTIE: PS50015; TWPR.NGFR.1; 1.
VARRANT 157 187; S -> T. VARRANT 157 S -> T. VARRANT 1
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DEATH RECEPTOR FAS (APO-1/CD95).
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Best Local Similarity 100.0
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hes 10; Conservative
Weiss W.R., Ansari A.A.;
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Q9GK36
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                                                                                                                                                                                                                                                        Macaca assamensis (Assam's macaque) (Assam's monkey),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Chi L., Shui B., Jiang H., He F.O., Zhang Y.R., Cai Y.Y.;
"Cloning and sequencing of bear monkey Fas antigen cDNN.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AF326208; AA64382.1;
R HSSP: PD5445; IDDF.
R InterPro; IPR001488; Death.
R InterPro; IPR001488; Death.
R SMART; SM00209; TNFR.C6; 2.
R SMART; SM00209; DEATH.1.
R SMART; SM00208; TNFR, 2.
R PROSITE; PS50017; DEATH_DOMAIN; 1.
R PROSITE; PS50017; DEATH_DOMAIN; 1.
R PROSITE; PS50050; TNFR_NGFR_1; 1.
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                                                                          Created)
Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN CD95.
331 AA
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PRT;
                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, FAS ANTIGEN APO-1/CD95.
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Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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    Cercopithecinae; Macaca.
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              NCBI_TaxID=9544;
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MEDLINE-21883618; PubMed-11491535;

Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,

Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,

Weiss W.R., Ansarik P.,

"Cloning, sequencing, and homology analysis of nonhuman primate

"Fast/Fas ligand and co-stimulatory molecules.";

"Manunogenetics 53:315-328(2001).

"RESP: P25445; DDF.

"RESP: P25445; DDF.

"InterPro; IPR001368; TNFR_C6.

"PROMOTO: PR001368; TNFR_C6.

"PROMOTO: DEATH: 1.

"SMART; SM00005; TNFR_C6.

"PROSITE: PS50015; TNFR_NGFR_1; 1.

"PROSITE: PS50050; TNFR_NGFR_1; 1.

"PROSITE: PS50050; TNFR_NGFR_1; 1.

"PROSITE: PS50050; TNFR_NGFR_2; 2.

"PROSITE: PS50050; TNFR_NGFR_2; 2.

"PROSITE: PS50050; TNFR_NGFR_2; 2.
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                                                                                                                                                                                                                                                                                                       Macaca nemestrina (Pig-tailed macaque).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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R -> H.
R -> S.
E -> G.
G -> A.
E -> G.
C -> A.
E -> G.
M. ID843C4DEID343F4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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60 R
61 N
77 E
95 G
282 E
298 G
300 C
37277 MW;
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NCBI_TaxID-9545;
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 60
61
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331 AA;
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RM 5010RECE FROM N.A.

RAM SEQUENCE FROM N.A.

RAM WELLING-2193181; PubMed-11491535;

RAM WELLING-2193181; PubMed-11491535;

RAM WELLING-2193181; PubMed-11491535;

RESIDENCE STAINS AND THE CO-STRUMLARCY MOLECULES.";

RESIDENCE STAINS AND THE COMPANY OF MISSINGLES.

ON THE CO-STRUMLARCY MOLECULES. THE CO-STRUMLARCY MOLECULES.";

RESIDENCE STAINS AND THE CO-STRUMLARCY MOLECULES.";

RESIDENCE STAINS AND
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Gaps

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RESULT 12 Q9DCQ1

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ENDURENCE FROM N.A.

ISONO T., Tanbe Y., Nagano Y., Seto A.;

Splicing and allelic variation in the rabbit Fas antigen gene.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AB021297; BAA78429.1; -.

HNSSP; 014763; 104V.

InterPro; IPR001368; TNFR_c6.

Pfam; PR00020; TNFR_c6; 3.

SMART; SM00208; TNFR_c6; 3.

SMART; SM00208; TNFR_R, GFR_1; UNKNOWN_1.

PROSITE; PS00065; TNFR_GFR_1; UNKNOWN_1.

SEQUENCE 263 AA; 30374 MW; 6D76782ABED1BFD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isono T., Tanbe Y., Nagano Y., Seto A.;

"Splicing and allelic variation in the rabbit Fas antigen gene.";

"Splicing and allelic variation in the rabbit Fas antigen gene.";

"Splicing and allelic variation in the rabbit Fas antigen gene.";

EMBL; AB021298; BAA78430.1; -.

HSSP, P25445; IDDF.

InterPro: IPR00288; Death.

InterPro: IPR001368; TNFR_c6.
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 263;
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100.0%; Pred. No. 0.041;
iive 0; Mismatches 0; Indels
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     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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6D76782ADED1BFD7 CRC64;
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06FA0033B1846591 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B-TYPE FAS ANTIGEN.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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Pred. No. 0.048;
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100.0%; Pred. NO. 0.048;
iive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 AA.
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEGUIENCE 319 AA; 35961 MW; 06FA0033B1
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Pfam; PF00531; death; 1.
Pfam; PF00053; TNFR_c6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00006; TNFR; 3.
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09XS60;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGES SPLICED VARIANT.
0ryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Haysshizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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88.9%; Pred. No. 0.02;
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PROSITE; PS00652; TNRFLNGFE_1; 1.
PROSITE; PS00650; TNRFLNGFE_2; 2.
SEQUENCE 327 AA; 37437 MW; D8DA95CA525CED56 CRC64;
                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER
                                                                                                                               327 AA
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                                                                                                                               PRT;
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STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; Pubmed-11217851;
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InterPro; IPR000488; Death.
InterPro; IPR001368; TWFR_C6.
Pfam; PF00020; TWFR_C6; 3.
SWART; SW0005; DEATH; 1.
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HSSP; P25445; 1DDF.
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Q9XS60
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A PAC AC OC OC OC OC

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE C-TYPE RSA SAWIGEN.

OC CHYPER RSA SAWIGEN.

OC CONTOCLOGUES CURL (Rabbit).

OC BUKARYOLDS BAS AWIGEN.

OC Mammalia: Eutheria: Lagomorpha; Leporidae; Oryctolagus.

OC Mammalia: Eutheria: Lagomorpha; Leporidae; Oryctolagus.

OC Mammalia: Eutheria: Lagomorpha; Leporidae; Oryctolagus.

OC NCBI_TAID=9986;

RN [1]

RN SQUENCE FROM N.A.

RA ISONO T., Tanbe Y., Nagano Y., Seto A.;

RI Spolicing and allelic variation in the rabbit Fas antigen gene.";

RN ISONO T., Tanbe Y., Nagano Y., Seto A.;

REMBL; AB021296; BAA78431.1; -.

DR EMBL; AB021299; BAA78431.1; -.

DR EMBL; AB021299; BAA78428.1; -.

DR EMBL; AB021299; BAA78428.1; -.

DR InterPro: IRR00488; Death.

DR InterPro: IRR00488; Death.

DR InterPro: IRR00489; Death.

DR PAGNITE: PSSOUGS THER_C6.

DR PAMRT; SM00208; THER_C6.

DR SMART; SM00208; THER_C6.

DR PROSITE: PSSOUGS; THER_MGFR.1; UNKNOWN.1.

DR PROSITE: PSSOUGS; THER_MGFR.2; 2.

SQUENCE 320 AA; 36102 MW; DA235E243220FEB3 CRC64;

QUEST MATCH SMILIARITY 100.0%; Pred. No. 0.048;

MATCHES 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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3 QNTKCRCK 10 |||||||| 108 QNTKCRCK 115

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GenCore version Copyright (c) 1993 - 2000

- protein search, using sw model OM protein

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Scoring table:

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747574 seqs, 111073796 residues Searched:

747574

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Anti-Fas humanised	Anti-Fas MAb HFE7A	Mouse anti-Fas ant	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas				
QI	AAW83031	AAW83032	AAW83033	AAW83034	AAW83035	AAW83042	AAB14748	AAB14772	AAB14773	AAB14774	AAB14777
DB	19	19	19	19	13	19	21	21	21	21	21
Query Watch Length DB	238	238	238	238	238	238	238	238	238	238	238
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	205	205	205	205	205	205	205	205	205	205	205
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### ALIGNMENTS

RESULT AAW83031

AAW83031 standard; Protein; 238 AA.

AAW83031;

15-MAR-1999 (first entry)

Anti-Fas humanised antibody HFE7A light chain HH type.

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFP7A; autoimmune disease; He87himoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; perniclous anaemia; Addison's disease; 

scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; Insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; qlomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Homo sapiens. Synthetic.

ocation/Qualifiers Peptide

/label- Sig\_peptide 21..28 /label- Mat\_protein 21..131 /label- Variable 132..238 /label= Constant Protein Region Region

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chain of murine anti-human Fast and antibody HFETA.

Chain of murine anti-human Esquence (see AAM83042) entailed making P47A, K49R, H80S, P81R, V82L, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSGHH7 SANK 73497 harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised HH type HFETA light chain and DNA encoding the region of human communoglobulin kappa chain, and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFETA approxasing has a capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting are used to evaluate, in animal models, treatments of diseases that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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S, Shin Y, Tohru T;
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44..58
/abal-CDR_L11
/note="claim 9"
74.80
/label-CDR_L2
/note="claim 9"
113..121
/label-CDR_L3
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KW apoptosis; HEPTA; autoimmune disease; Hashimoto's disease; KW systemic lupus erythematosus; graft versus host disease; KW systemic lupus erythematosus; graft versus host disease; KW sjogren syndrome; pernicious anaemia; Addiseon's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; W rheumatoid arthritis; autoimmune haemolytic anaemia; W myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; W atopy; arteriosclerosis; myocarditis; cardiomyopathy; W glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Anti-Fas humanised antibody HFE7A light chain HM type.

(first entry)

15-MAR-1999

AAW83032;

AAW83032 standard; Protein; 238 AA.

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AAW83032 RESULT

104 padfavyycqqsnedprt 121

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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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Nobufusa S, Shin Y, Tohru T;
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/label- Mat_protein
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Gaps

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100.0%; Score 205; DB 19; Length 238; 39.7%; Pred. No. 1.2e-05; tive 47; Mismatches 0; Indels 0

Conservative

Query Match Best Local Similarity Matches 31; Conserv

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         this is the antino acid sequence of the HW Type numanisaci light chains of murine anti-human peaguence (see AAW83042) entailed making than of murine anti-human sequence (see AAW83042) entailed making than an of the murine sequence (see AAW83042) entailed making conserved in the human light (kappa) chain. Host cell E. coll pHSGHM17 SANK 73597 harbors plasmid pHSGHM17 carrying a fusion of fragment of the humanised HW type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6702 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised antibodies by culturing host errors are capable of inducing apoptosis in abnormal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune interactions, and also to treat such diseases, including autoimmune capables of systemic lupus erythematosus, Hashimoto's disease, classes, solaroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthrilis, autoimmune haemolytic anaemia, disease, short disease, alutinimune haemolytic anaemia, disease, short disease, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune haemoly
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This is the amino acid sequence of the HM type humanised light
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Pred. No. 1.2e-05;
47; Mismatches 0;
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/label= Mat_protein
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Matches 31; Conserva
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This is the amino acid sequence of the MM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli saw 73697 harbors plasmid pHSGMMG carrying a fusion fragment of the humanised MM type HFE7A light chain and DNA encoding the region of human kappa chain, and is deposited as FERM BP-6071 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), clike native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
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Masahiko O, Nobufusa S, Shin Y, Tohru T;
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                       .32..238
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/label= CDR_L3
/note= "claim 9"
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label= CDR_L1
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Best Local Similarity
Matches 31; Conserv
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104 eedaatyycqqsnedprt 121

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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                              HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic luque serythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephitis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                            Anti-Fas humanised antibody HFE7A light chain PDHH type.
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S, Shin Y, Tohru T;
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'label= Sig_peptide
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/label- Mat_protein
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                      AAW83034 standard; Protein; 238 AA.
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label= Variable
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/label- Constant
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Synthetic.
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Masahiko O,
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            AAW83034
RESULT
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chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49R, H805, P81R, V82L, E84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSHS SANK 70398 harbors plasmid pHSHH5 carrying a fusion fragment of the humanised PHH type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERN BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host methods for producing humanised antibodies by culturing host ells. Humanised versions of HFE7A (see AAM8301-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autcimmune classes (e.g. systemic lupus erythematosus, Hashimoto's disease, classes, slocknowe, pernicious anaemia, disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
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/label= Mat_protein
21..131
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Synthetic.
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CHain of murine anti-human Fas monoclonal antibody HFE7A.

CHAIN (A PR and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host call Escherichia coli pHSHM2 SANK 7019B harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERW BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host calls. Humanised versions of HFE7A (see AAW83031-37), like native KFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas,Fas ligand
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S, Shin Y, Tohru T;
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                                                                                                                                             /note= "claim 9"
74..80
/label= CDR_L2
label- Variable
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                                                                                                                                                                                                                                            "claim 9"
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/label= CDR_L1
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N-PSDB; AAV70078.
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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S, Shin Y, Tohru T;
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/label= CDR_L1
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97JP-0169088.
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15-MAR-1999 (first entry)
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                                                                                                                                                                                       This is the amino actor to the tripe condition of the light chain was obtained from HEPA-secreting hybridoma (FERM BP-5828)

RNA by RT-PCR (See AAV70127-28). The invention provideds humanised HFBA antibodies (see AAV70127-28). The invention provideds humanised HFBTA antibodies (see AAW8301-37) produced by CDR grafting. These antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, scleroderma, Goodpasture syndrome, Crohn's disease, thematoid arthitis, autoimmen haemolytic anaemia, sterility, myasthenia purpura and insulin-dependent diabetes). allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
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                                                   Reference Example 4; Page 189-190; 292pp; English.
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                                                                  The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
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Example 4; Page 70; 139pp; Japanese.
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                                                        (complementarity determining regions) to antibody HEE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apotosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, glomerulonephritis, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
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47; Mismatches 0
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antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
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Best Local Similarity
Matches 31; Conserv
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interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, and organ graft is, aplastic anaemia (pannyalophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and ABB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
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7; Mismatches
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39.7%; F
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Chimeric - Homo sapiens.
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               glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
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 cardiomyopathy,
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myocarditis,
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39.7%; Pred. No. 1.2e-05;
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   allergy, atopy, arteriosclerosis,
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                                                                                                                                                                                                                                                                                                                                                               Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; antialergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-arthritic, anti-thritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyronimetic, antirity antirheumatic, nephrotropic, antilefrality, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
represent the light chains of several humanised {\tt HFE7A}-derived anti-Fasantibodies.
                                                                                                                                             Gaps
                                                                                                                               Tamaki I, Takahashi T;
                                                                                 Length 238;
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                                                                               DB 21;
                                                                              100.0%; Score 205; DB 21
39.7%; Pred. No. 1.2e-05;
ive 47; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
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N-PSDB; AAA11547.
                                                                                            Similarity
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antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or Inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft cersus host disease, Sjorgen's Syndrome, Pernicious or hypoplastic anemia, Addison's disease, soleroderma, Goodpasture syndrome, Conn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, anlitple Sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (1) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the native ligand, do not induce liver site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of murine anti-Fas monoclonal antibody HED7A light chain described in the
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39.7%; Pred. No. 1.2e-05;
ive 47; Mismatches 0;
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30-SEP-1998;
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cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                       This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents capoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, cantidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgem s syndrome, pernicious or hypoplastic versus host disease, slorederma, Goodpasture syndrome, Codisease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (S, C or D) or alcoholic), and transplant rejectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic mutive liqand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody HERPA light chain HH type which is used in the method described in the invention.
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                                                                   New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
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                                                                                                                                                                       Example reference 14; Page 114-115; 263pp; English.
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7; Mismatches 0;
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39.7%; P
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                      N-PSDB; AAA11562
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This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas (1 igand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antitheumatic, nephrotropica, immunosuppressive, thyromimetic, antitheumatic, nephrotropic, antidinfertility, neuroprotective, antitheumatic, nephrotropic, antiding (1) are used to treat and/or prevent consists by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive consmina, Addison's disease, soleroderme, permicious or hypoplastic versus host disease, soleroderme, goodpasture syndrome, consmina, Addison's disease, soleroderme, goodpasture syndrome, consmina, autoimmune hemolytic anemia, sterility, myasthenia gravis, myocarditis, multiple solerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral) (6, c or b) or alcoholic), and transplant rejection. (1) selectively contined disease models. (1) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fass antibody response. This sequence represents a humanised anti-Fass antibody response. This sequence represents
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:17:02; Search time 82.88 Seconds (without alignments) 22.987 Million cell updates/sec

5\_G\_6\_G\_7 205 Title: Perfect score:

Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 231628 seqs, 24425594 residues

Searched:

231628

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 73, Appl	73,	58,	Sequence 58, Appl	7	6	ģ	9	Sequence 8, Appli	16,	Sequence 51, Appl	14,	18,	7	14,	Sequence 14, Appl	Sequence 24, Appl	24,	Sequence 24, Appl	9	9	9	10,	10,	10,	13,	9,
SUMMARIES	ID	US-08-483-636-73	US-08-483-632-73	US-08-483-636-58	US-08-483-632-58	US-08-483-636-2	US-08-483-632-2	US-08-466-151-6	US-08-466-163B-6	US-08-491-845-8	US-08-491-845-16	US-08-513-968-51	US-08-579-378A-14	US-08-579-378A-18	PCT-US96-13152-2	US-08-483-636-14	US-08-483-632-14	US-08-111-080-24	US-08-211-980-24	PCT-US93-07967-24	US-08-887-352B-6	US-09-109-207C-6	US-09-296-005-6	US-08-887-352B-10	US-09-109-207C-10	US-09-296-005-10	US-08-887-352B-13	US-08-466-151-9
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	Score M	198	198	198	198	198	198	197	197	197	197	197	197	197	197	195	195	184	184	184	182	182	182	182	182	182	182	182
	Result No.	1	7	ж	4	2	9	7	œ	6	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

PILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATORNEY/AGENT INFORMATION:
NAME: SULTON, JOFÍTEY A.
REGISTRATION NUMBER: 94,028
REFERENCE/DOCKET NUMBER: 950186-3
FILECOMMUNICATION INFORMATION:
TELEPAN: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single

28	182	888	218	4 4	US-09-109-207C-13 US-09-296-005-13	Sequence 13,	App]
000	182	88.8	218	4	-08-466-163B-	6	Appli
3.1 2.2	178		111	7 m	US-U8-88/-352B-5 RS-08-466-151-2	Sequence 5, A	App1.
1 E	178		111	) <del>4</del>	-09-109	'n	Appli
34	178		111	4	US-09-296-005-5	S,	App1
35	178		111	4	US-08-466-163B-2	, '	Appli
36	178		114	~	US-08-887-352B-9	ο, α	Appli
3,4 3,8	175		114	4 <	US-U9-109-20/C-9		Appli
0 6	165		239	* ~	US-08-553-497A-18	, 6	Appl
40	159		114	0	-08-887-352B-8	8	Appli
41	159		218	4	US-09-282-505-1	1,	App1 i
42	159		218	4	-09-054-255-1	ì,	Appli
43	156	76.1	114	٠ ب	-09-109-207C	ω α	Appli
44	156	76.1 76.1	218	4 2	US-09-296-005-8 US-08-887-352B-15	Sequence 8, P Sequence 15,	Appli App]
					ALIGNMENTS		
RESULT	7						
US-08-483	3-636-73	8					
; Sequenc	se 73, 1	Sequence 73, Application		80	US/08483636		
; Patent	NO. 59.	atent No. 5914IIU GENERAL INFORMATION:					
APPI	ICANT	Holmes.	s. Stephen	hen	D.		
, APPI	APPLICANT:		- 57:	e11			
; APPI	APPLICANT:	Sylves	er	anie			
ILIL ' .	E OF I	TITLE OF INVENTION:		QIIIO	Recombinant IL4 Antibodies Useful	ul in	
ITIT ;	LE OF II	TITLE OF INVENTION:		atme	Treatment of IL4 Mediated Disorders	ders	
INCON.	ESPOND!	NOMBER OF SECTENCES: /	· · ·				
, ,	ADDRESSEE:	E: Smit	hKline	Bee	SmithKline Beecham Corp./Corporate		
, AI	DRESSE		Intellectual	a)	Property		
:	۰	P.O. Box	153	\	JW2220		
		g of	Prussia				
: :	STATE:	PA					
 	COUNTRY: 7.197	KY: USA 19406-0939	•				
COME	UTER RI	COMPUTER READABLE FORM:	FORM:				
. ME	MEDIUM T	TYPE: F]	Floppy disk	isk			
	COMPUTER:	: IBM PC	O	atik	compatible		
5 6	ERAL IN	"	ď		3-DOS		
	SOFTWAKE:	7	Patentin Release	teas			
A P	PLICAT	APPLICATION NIMBER:	ER: II	30/8	IIS 708 7483 . 636		
G	FILING DATE	ATE:					
	TOTAL CHARGE		707				

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0; Gaps
                                              1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXXABSNLESXXXXXXXXXXXXXXXXXXX 60
                                                                        24 KASQSVDYDGDSYXMNWYQQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTFTISSLQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 131;
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: STVESTER, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Intellectual Property CREET: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.6%; Score 198; DB 2; 38.5%; Pred. No. 5.1e-08; tive 47; Mismatches 1
  47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-007-1993
FRICK DATE: 14-007-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-007-1993
PRIOR APPLICATION DATA:
FILING DATE: 07-5EP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sutton, Jeffrey A.
REGISTATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEPHONE: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                              84 PEDIATYYCQQSNEDPPT 101
    Conservative
                                                                                                                                       61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 131 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 38.5
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-483-636-58
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  30;
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    Matches
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                                                                                                                                                                                1 KASQSVDYDGDSYMNXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                          24 KASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTFTISSLQ 83
                                                                                      ; Score 198; DB 2; Length 111;
; Pred. No. 3.1e-08;
47; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Treflectual Property CTRET: P.O. Box 1539 / UW2220 CTTY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 198; DB 2;
Pred. No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07.5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-5EP-1994
ATTORNEY.AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028 REFERENCE/DOCKET NUMBER: P50186-3 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 73, Application US/08483632 Patent No. 5928904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                      96.6%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.68;
38.58;
                                                                                                                                                                                                                                                                                              84 PEDIATYYCQQSNEDPPT 101
                                                                                                                                                                                                                                                                    61 XXXXXXXXQQSNEDPRT 78
                                                                                                             Best Local Similarity 38.59
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
; MOLECULE TYPE:
US-08-483-636-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-483-632-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-483-632-73
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                                                                                        Query Match
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44 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 132;
                                           APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant LL4 Antibodies Useful in TITLE OF INVENTION: Treatment of LL4 Mediated Disorders NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant LL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of LL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                         NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 198; DB 2;
; Pred. No. 5.2e-08;
47; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
                                                                                                                                                                                                                                                                                                                          ZIP: 19406-0039
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFFWARE: Patentin Releases ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-483-632-2
Sequence 2, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.6%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEDAATYYCQQSNEDPPT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.5%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-483-636-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                            GENERAL INFORMATION:
       Patent No. 5914110
                                                                                                                                                                                                                                                                                                         PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
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                                                                                                                                 Sequence 58, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II4 Antibodies Useful in TITLE OF INVENTION: Treatment of II4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property TreErr: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.6%; Score 198; DB 2; 38.5%; Pred. No. 5.1e-08; iive 47; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
ATTORNER: SILLING DATE: 07-SEP-1994
ATTORNER: SILLING DATE: 07-SEP-1994
ATTORNER: SILLING NUMBER: SILLING DATE: 07-SEP-1994
ATTORNER: SILLING NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08483636
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103 AEDVAVYYCQQSNEDPPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEDVAVYYCQQSNEDPPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 XXXXXXXXQQSNEDPRT 78
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Best Local Similarity 38.54
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                           RESULT 4
US-08-483-632-58
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US-08-483-636-2
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24 KASQSVDYDGDSYMNWYQQRPQQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.1%; Score 197; DB 3;
illarity 38.5%; Pred. No. 3.3e-08;
Conservative 47; Mismatches 1.
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US 08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR PILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR RILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
APPLICATION NUMBER: 08/466163
APPLICATION NUMBER: 08/405617
FILING DATE: 15-WAR-1995
FILING DATE: 15-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA: 07/879495
FILING DATE: 07-WAY-1992
PRIOR APPLICATION DATA: 07/879495
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/74768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
RMEESTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 99,044
                                                                                                                    APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
                                                  SYSTEM: PC-DOS/MS-DOS WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08466163B Patent No. 6329509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 EEDAATYYCQQSNEDPFT 101
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                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 30; Conserva
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LENGTH: 106
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                                                                                                                                                             COUNTY FOR COUNTY FOR COUNTY FOR COUNTY FOR COUNTY FOR COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BAS #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: PCT-10/93
FILING DATE: 14-OCT-1993
FILING DATE: 17-OCT-1993
FILING DATE: 17-OCT-1993
FILING DATE: 07-SEP-1993
FILING DATE: 07-SEP-1994
ATTONNEY/AGENT INFORMATION:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE Genentech, Inc.
STREET: I DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215, 270-5024
TELEFAX: (215, 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STATE: California
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.5%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
  NUMBER OF SEQUENCES:
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US-08-466-151-6
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1 KASQSVDYDGDSYMNXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.1%; Score 197; DB 1; Length 111; 38.5%; Pred. No. 3.7e-08; ive 47; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, KIyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MAEDA=5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      Sequence 16, Application US/08491845
Patent No. 5773247
GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: EDA, YASUYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-513-968-51; Sequence 51, Application US/08513968; Patent No. 6114143; Patent No. 6114143; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
                                                               84 EEDGATYYCQQSNEDPWT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 PEDIATYYCQQSNEDPWT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 XXXXXXXXQQSNEDPRT 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-491-845-16
                                  61 XXXXXXXXQQSNEDPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C. COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                    RESULT 10
US-08-491-845-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                  δλ
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                                                                                                                                                                                                                                             1 KASQSVDYDGDSYMNXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXXXXX
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                                                                                                                           Length 106;
                                                                                                                 96.1%; Score 197; DB 4; Length 10
38.5%; Pred. No. 3.3e-08;
.ive 47; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EDA, Yasuyuki
APPLICANT: SHIOSAKI, Koulichi
APPLICANT: SHIOSAKI, Koulichi
APPLICANT: TOKIYOSHI, Kayoshi
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.1%; Score 197; DB 1; 38.5%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MAEDA=5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08491845
Patent No. 5773247
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TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                 84 EEDAATYYCQQSNEDPFT 101
                                                                                                     Ouery Match
Best Local Similarity 38.5%
Matches 30; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Conservative
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; ORGANISM: Mus musculus US-08-466-163B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-491-845-8
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44 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08579378A
Sequence 18, Application US/08579378A
Sequence 18, Application US/08579378A
Sequence 18, Application US/08579378A
SEQUENCE CO, Man Sung
TITLE OF INVERVION: Humanized Antibodies Reactive with
TITLE OF INVERVION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend and Crew
One MarketPlaza, Steuart Tower, Suite 2000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                   ZIP: 94105

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURREWY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

96.1%; Score 197; DB 4;
Best Local Similarity 38.5%; Pred. No. 6.2e-08;
Matches 30; Conservative 47; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11823-002220
                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
FILING DATE: 19-SEP-1995
FILING DATE: 19-SEP-1995
                                                                                                                                                                       UMBER: US/08/579,378A
27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Liebescheutz, Joe O. REGISTRATION NUMBER: 37,505 REFERENCE/DOCKET NUMBER: 116 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 EEDAATYYCQQSNEDPWT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-579-378A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One MarketPl
CITY: San Francisco
STATE: California
                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 27-DEC
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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US-08-579-378A-14

Sequence 14, Application US/08579378A

Patent No. 6210671

GENERAL INFORMATION:
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
STREET: One Marketplaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 96.1%; Score 197; DB 3; Length 115; Best Local Similarity 38.5%; Pred. No. 4.2e-08; Matches 30; Conservative 47; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FLING DATE: 11-SEP-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PARESTERMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                       APPLICANT: OSATOMI, KIYOSAII
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                 BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
TENGTH: 115 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                           MAKIZUMI, Keiichi
SHIOSAKI, Kouichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 PEDIATYYCQQSNEDPWT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 115 amino acids
amino acid
3X: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 XXXXXXXXQQSNEDPRT 78
EDA, Yasuyuki
MAEDA, Hiroak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: ONE MAL....
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-513-968-51
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                              20004
                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II.4 Antibodies Useful in TITLE OF INVENTION: Treatment of II.4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                      APPLICATION NUMBER: BP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 STREET: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.1%; Score 197; DB 5; 38.5%; Pred. No. 2.9e-07; iive 47; Mismatches 1
       17-Aug-95
JMBER: EP 95 114 969.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCI/US/94/10308
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PROR APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08483636; Patent No. 5914110; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 PEDFATYYCQQSNEDPWT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.1%
Best Local Similarity 38.5%
Matches 30; Conservative
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS: LENGTH: 218
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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GENERAL INFORMATION:
    APPLICANT: Martin, Ulrich, et al.
    TITLE OF INVENTION: Atti-selectin antibodies for prevention of multiple organ fai
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Attn: Norman D. Hanson
    STREET: 805 Third Avenue
    CITY: New York
    STATE: New York
    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.1%; Score 197; DB 4; Length 13
38.5%; Pred. No. 6.2e-08;
11ve 47; Mismatches 1; Indels
                                                             CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AGG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 17-AGG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Libescheutz, Jo-6.
REGISTRATION NUMBER: 37,505
REGISTRATION LONGRAFION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE ATGS-22400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP 95 112 895.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 PEDFATYYCQOSNEDPWT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.55
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
PCT-US96-13152-2
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| REFERENCE/DOCKET NUMBER: P50186-3
| TELECOMMUNICATION INFORMATION:
| TELEPHONE: (215) 270-5024
| TOPOLGY: (215
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:18:57; Search time 108.64 Seconds (without alignments) 68.989 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

5\_G\_6\_G\_7 205\_ARSQSVDVDGDSYMNXXXXX.....XXXXXXXXXXXQQSNEDPRT 78

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		Kappa	kappa cha			kappa		kappa	kappa	Ig kappa chain V r	Ig kappa chain V-J	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain V r	anti-glycoprotein	б	р		ь	g light	ь	ь	ь	ь	ь	ь	ь	ь	g kappa cha	Б
SUMMARIES	ID		NVMS63	KVMS43	KVMS69	A38601	KVMS08	S42193	S19971	PH1226	KVMSC1	996608	KVMS10	S19976	S19972	D45722	S26344	KVMS37	S26343	KVMSM6	B49442	863596	KVMS84	809965	KVMS32	PH0093	PH1079	PL0081	506731	KVMS80	KVMS54
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	Query Match Length	11 -	777	111	111	66	111	81	112	131	111	111	110	112	112	111	107	111	107	131	96	115	111	111	132	109	102	111	120	111	108
dР	Query		0.00	96.1	96.1	94.1	94.1	93.2	92.7	92.7	91.2	87.3	84.1	83.9	79.0	9.92	75.6	75.6	75.1	73.7	72.7	71.7	8.99	66.3	66.3	62.3	64.9	64.9	64.9	64.4	63.4
	Score	1 0	0 10	161	197	193	193	191	190	190	187	-	172.5	172	162	157	155	155	154	151	149	147	137	136	136	135	133	133	133	132	130
	Result No.		<b>-</b> (	7	m	4	'n	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT KVMS43

Nature 101-September chain V region (PC7043) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000
C; Accession: A01937; S42187; S42184; S42189; S42187; MUID:94009207

Ig kappa chain V r	Ig kappa chain V-J	Ig kappa chain V a	Ig kappa chain pre	Ig light chain V r	Ig kappa chain V-J	Ig kappa chain V r	Ig kappa chain - h	Ig kappa chain V r	monoclonal antibod	Ig kappa chain V r	kappa	_			
KVMS75	808963	E53285	S06732	PH1076	808969	A56169	KVMS40	S37202	S45715	S40331	KVMS85	JC5810	KVMS50	S68241	B49047
п,	7	1 2	0	2	1 2	0 2	1	1 2	2 2	3 2	1	8	1 1	8	8
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63.4	63.	63.	63.	62.	62.	62.	62.	62.	62.	62.	61.	90.	.09	59.	58.
130	130	130	130	129	129	129	127	127	127	127	125	124	123	121	120
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT KVMS83	JLT 1 583
Igi	Ig kappa chain V region (PC7183) - mouse
c;s	C;Species: Mus musculus (house mouse)
C;D	C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; A	C; Accession: B01937; A01937
R; W	R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nati	Nature 276, 785-790, 1978
A; T	A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; R	A; Reference number: A93204; MUID: 79073152
A; A	A;Accession: B01937
A; W	A; Molecule type: protein
A; R	A; Residues: 1-111 <we1></we1>
ŭ Ü	C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hai	n disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
ເຊ : ວ	C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; K	C;Keywords: heterotetramer; immunoglobulin
F; 1	F;16-94/Domain: immunoglobulin homology <imm></imm>
F; 2.	F;23-92/Disulfide bonds: #status predicted
Õ	Jery Match 96.6%; Score 198; DB 1; Length 111;
'n	Similarity 38.5%; Pred. No. 2.2e-09;
Ĕ	o; caps
QY	1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXX 60
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2	יייייייייייייייייייייייייייייייייייייי
Qy	61 XXXXXXXXQQSNEDPRT 78
,	
αΩ	84 EEDAATYYCQQSNEDPLT 101

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If kappa chain V region (PC6308) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; Accession: C01937, A01937
Nature 276, 785-790, 1978
N; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
N; Reference number: A9304; MUD: 79073152
A; Accession: C01937
A; Accession: C01937
A; Residues: 1-111 <WEI>C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer simmunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Typecies: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; States: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C; Accession: A38601
R; Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A; Title: Common structural features among monoclonal antibodies binding the same anti A; Reference number: A38601; MuID: 91115823
A; Reference number: A38601
A; Accession: A38601
A; Molecule type: mRNA
A; Residues: 1-93 <GOS>
A; Residues: 1-93 <GOS>
A; Csuperfemily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
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                                                                                     Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.1%; Score 193; DB 2;
llarity 37.2%; Pred. No. 5.4e-09;
Conservative 47; Mismatches 2;
                                                                                     Score 197; DB 1;
Pred. No. 2.8e-09;
                                                                                                                                                   47; Mismatches
F;23-92/Disulfide bonds: #status predicted
                                                                                        96.1%;
38.5%;
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                                                                                                                                                                                                                                                                                                                                                  61 XXXXXXXXQQSNEDPRT 78
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Best Local Similarity 37.2%
Matches 29; Conservative
                                                                                                                                                          Conservative
                                                                                        Query Match
Best Local Similarity
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Matches 29; Conserv
                                                                                                                                                       30;
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A; Cross-references: EMBL:225454; NID:9407842; PIDN:CAB80941.1; PID:9407843
A; Note: V. Kappa-21E; anti-collagen
C; Complex: An immunoglobulin heteroternamer subunit consists of two identical light (kappa: Superfamily: Immunoglobulin vegton; immunoglobulin homology
C; Superfamily: Immunoglobulin V region; immunoglobulin homology
F; Reywords: heteroternamer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology < TMM>
F; 23-92/Disulfide bonds: #status predicted
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Focession: E01397
A;Molecule type: protein
A;Residues: 1-111 <WEI>
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A; Residues: 12-99 <MOZ>
A; Cross references: EMBL:225446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A; Note: V. Kappa-21E; anti-collagen
A; Accession: 542191
A; Molecule type: DNA
A; Residues: 10-99 <MOY>
A; Cross references: EMBL:225452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A; Note: V. Kappa-21E; anti-collagen
A; Accession: 542192
                          A;Residues: 10-99 <MOJ>
A;Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                              A;Cross-references: EMBL:225458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A;Note: V-kappa-21E; anti-collagen
A;Accession: 542190
                                                                                                                                                                                                                                                                                                                                                                     A;Cross.references: EMBL:225450; NID:g407838; PIDN:CAA80937.1; PID:g407839 A;Note: V-kappa-21E; anti-collagen A;Note: V-kappa-21E; anti-collagen A;Note: U-kappa-1289 A;Accession: 642189 A;Nolecule type: DNA A;Residues: 15-99 <moa>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:225448; NID:9407836; PIDN:CAA80935.1; PID:9407837
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42188
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nes 30; Conserv
                                                                                                                                                A; Molecule type: DNA
A; Residues: 12-99 <MOW>
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 13-99 <MOF>
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A; Residues: 10-99 <MOO>
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Matches
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R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; I Gene 121, 271-278, 1992
As,Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A;Reference number: PH1224; MUID:93077041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S50265; NID:9260765; PIDN:AAB24320.1; PID:9260766
A;Note: this mouse sequence was hybridized and fused with a human constant region gen
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exappa chain V region (CBPC 101) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C;Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related A;Reference number: A93822; MUID:79012520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Wolecule type: protein
A; Residues: 1-111 <MCK>
C; Comment: This chain was isolated from a myeloma protein.
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                                    Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 KASQSLDYDGDSYMWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 103
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24 KASQSLDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: heterotetramer; immunoglobulin
F1-12/Domain: signal sequence #status predicted <SIG>
F;21-131/Product: Ig light chain V region #status predicted <WAT>
F;36-114/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.8e-08;
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Pred. No. 2:9e-08;
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F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
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1 Similarity 35.9%;
28; Conservative 4
                                                                               EEDAATYYCQQSSEDPPT 101
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                                                     61 XXXXXXXXQQSNEDPRT
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Best Local Similarity
Matches 28; Conserv
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Best Local Similarity
Matches 28; Conserv
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A; Molecule type: mRNA
A; Residues: 1-131 <WEI>
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PH1226
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R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec A;Accession: 542193
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Bate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19971; S19973
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
                                                                                                                                                                                                                                                                                       Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:225456; NID:g407846; PIDN:CAA80943.1; PID:g407847 A;Note: the authors translated the codon GTT for residue 36 as Ala C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: attentetramer; immunoglobulin C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  9
                                                     83
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Fesidues: 1-112 <WEW>
A.Accession: 519973
A.Accession: 519973
A.Accession: 519973
A.Accession: 519973
A.Molecule type: mRNA
A.Residues: 1-112 <WEW>
A.Cross-references: EMED:X65092; NID:q52292; PIDN:CAA46220.1; PID:q52293
                                 24 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYTASNLESGIPARFSGSGSGTDFTLNIHPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYVASNLESGIPARFSGSGSGTDFTLNIHPVE
KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX
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C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heteroterramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 81;
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35.9%; Pred. No. 1.5e-08;
iive 49; Mismatches 1;
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; Pred. No. 7e-09;
47; Mismatches
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                                                                                                                                                        84 EEDAATYYCQQSNEDPWT 101
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Best Local Similarity 36.8°
Matches 28; Conservative
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                                                                                                        61 XXXXXXXXXQQSNEDPRT
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Best Local Similarity
Matches 28; Conserv
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A; Residues: 1-81 <MOJ>
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C;Accession: D45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A;Reference number: A45722; MUID:93100833
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep_1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 06Feb-1995 #sequence_revision 06Feb-1995 #text_change 21-Jan-2000
C;Date: 06Feb-1995 #sequence_revision 06Feb-1995 #text_change 21-Jan-2000
C;Accession: S19975 #tethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Reference number: S19963
A;Reference number: S19963
A;Reference number: S19972
A;Status: preliminary
Species: Mus musculus (house mouse)
Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 KASQSLDYDADSYMHWYQQKPGRPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA4621.1; PID:g52299 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin pomology F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>
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                                                                                         Ξ.Ρ.
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                                                 C; Accession: S19776
R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, B: Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, B: Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, B: Weissenhorn, Structural characterization of CD4 mAb.
A; Reference number: S19963
A; Accession: S19976
A; Accession: S19976
A; Accession: Lyeiminary
A; Molecule type: mRNA
A; Residues: 1-112 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 172; DB 2;
Pred. No. 9.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.9%; Scc. 32.1%; Pred. No. ...
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Matches 23; Conservative
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Best Local Similarity
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A; Residues: 1-112 <WEI>
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A; Mesidues: 1-110 
A; Residues: 1-110 
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology 
F; 16-94/Domain: immunoglobulin homology 
F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                   Ig kappa chain V-J region (1E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: 809966
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: 809955; MUID:90269328
A;Accession: 809966
A;Accession: 809966
A;Accession: 809966
A;Residues: 1-111 <REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (PC7210) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000 C; Accession: D01937, A01937 A01937 B; Weigert, M.; Gatumaitan, L.; Loh, E.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978 A; Weigert of genetic information may produce immunoglobulin diversity. A; Reference number: A93204; MUID:79073152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231 Cs.Superfamilly: immunoplobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-94/Domain: immunoglobulin homology <IMM>
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34.6%; Pred. No. 8.2e-07;
Live 48; Mismatches 2;
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Subsidence that we region - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C; Accession: 826344
A; Gille: Antibodies that are specific for a single amino acid interchange in a protein (A; Reference number: 826309; MuID:91341421
A; Title: Antibodies that are specific for a single amino acid interchange in a protein (A; Reference number: 826309; MuID:91341421
A; Accession: 82634
A; Accession: 82634
A; Accession: 82634
A; Residues: 1-107 <STA>
A; Molecule type: mRNA
A; Residues: 1-107 <STA>
A; Residues: 1-107 <STA>
A; Residues: 1-107 <STA>
A; Cross-references: EMBL: X59209; NID:952336; PIDN:CAA41919.1; PID:91334074
C; Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C; Reywords: heterotetramer; immunoglobulin homology <IMM>
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                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Rolecule type: nucleic acid A;Rolecule type: nucleic acid A;Rolecule type: nucleic acid A;Note: Sequence extracted from NCBI backbone (NCBIP:120592) C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: glycoprotein F;16-94/Domain: immunoglobulin homology <IMM>
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Matches 22; Conservative
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1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXX 60
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                        P01598
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P01628
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COMPLEMENTARITY-DETERMINING-2.
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15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region PC 7183.
Mus musculus (Mouse).
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KVIM_HUMAN
KV5N_MOUSE
KV3E_MOUSE
KV5J_MOUSE
KV3L_HUMAN
KV2A_MOUSE
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RV3M_MOUSE STANDARD; 1

AC PV3M_MOUSE STANDARD; 1

DT 21-JUL-1986 (Rel. 01, Created)
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PIR: B01937; KVM883.

HSSP; P01789. 1MCP.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PP00047; ig; 1.

Immunoglobulin V region.

DOMAIN 24 38 C

DOMAIN 39 53 F

DOMAIN 54 60 C

DOMAIN 54 60 C

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DOMAIN 61 92 F

DOMAIN 61 92 F
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             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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24 KASQSVDYDGDSYMNWYQQKPGQPPKVLIFAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE-79073152; PubMed-103003;
Medigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
Weispert M., Gatmaitan L., Information may produce immunoglobulin
Alvarsity.";
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                                                                                                                                                                                                    Length 111;
   COMPLEMENTARITY - DETERMINING - 1.
                                     COMPLEMENTARITY - DETERMINING - 2.
                                                                         COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                                                                  96.1%; Score 197; DB 1; L
38.5%; Pred. No. 8.1e-08;
Live 47; Mismatches 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 6308.
                                                                                            FRAMEWORK-4.
BY SIMILARITY.
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BY SIMILARI
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PIR; C01937; KVMSOB.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam; PR0047; Ig'. ISMART; SMO0406; IGV: 1
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                       84 EEDAATYYCQGSNEDPWT 101
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Best Local Similarity 38.58.
Matches 30; Conservative
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Matches 29; Conservative
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P01667;
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KV30_MOUSE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7043.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                              MEDINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.1%; Score 197; DB 1; Length 111; 38.5%; Pred. No. 8.1e-08; ive 47; Mismatches 1; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 Kappa chain V-III region PC 7769.
Mus musculus (Mouse).
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InterPro; IPR003596; Ig_v.
Pfam: PP00047; ig; 1.
SMART; SM00406; Igv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                  HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
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12002 |
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Nature 276:785-790(1978).
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Nature 276:785-790(1978).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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HSSP; P01789; 1MCP.
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Best Local Similarity
Matches 30; Conserv
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P01669;
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NCBI_TaxID=10090;
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21-JUL-1986
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P01660;
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                                                                                                                                                        McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN. HSSP; PO1789; IMCP.
InterPro; IPR003506; Ig.MC.
InterPro; IPR003596; Ig.V.
SMART; SM00406; Ig.1.
SMART; SM00406; IG.1.
Immunoglobulin V region.

23 FRAMEWORK-1.
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-19073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                          FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                       91.2%; Score 187; DB 1; Length 111; 35.9%; Pred. No. 5.8e-07; ive 48; Mismatches 2; Indels
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COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region CBPC 101.
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                                  KV3L_MOUSE
P01664;
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P01668;
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KV3P_MOUSE
                        KV3L_MOUSE
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Matches
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MEDLINE=79012520; PubMed=99744;

MEDLINE=79012520; PubMed=99744;

McKean D.J., Bell M., Potter M.;

Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S., 75:3913-3917(1978).

-1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 KASQSLDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Score 172.5; DB 1; Length 110; 34.6%; Pred. No. 9.7e-06; Live 48; Mismatches 2; Indels 1
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PIR; D01937; KVMS10.
HSSP; P01789; JMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SWART; SMO406; IGv; 1.
Immunogloblin V region.
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HSSP; P01789; 1MCP.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV: 1.
Immunoglobulin V region.
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Best Local Similarity 34.65
Matches 27; Conservative
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Best Loc Matches

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KV3J\_MOUSE

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24 RASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVE 83
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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                             Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY - DETERMINING - 2.
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COMPLEMENTARITY-DETERMINING-3.
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12005 MW; 39D87619313453CB CRC64;
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse)
                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 4050.
                                                                                                  111 AA.
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BY SIMILARITY.
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SEQUENCE OF 1-35.
MEDLINE-78235887; PubMed-98179;
                                                                                                                                                                                                                                                                                                                                                         Auture 276:885-790(1978).
PIR; A01935; KVNSM6.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
 84 ADDAATYYCQQNNEDPYT 101
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Best Local Similarity
Matches 21; Conserv
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P01663;
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MEDLINE=79012520; PubMed=99744;
MCKGan D.J., Bell M., Potter M.;
McKhanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                 Gaps
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                                                                                                                                                                   24 RASESVDSYGNSFWHWYQQKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVE 83
                                                                                                                                               24 RASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diversity.";
Nature 276:785-790(1978).
-!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (PC 9245).
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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;; Pred. No. 0.00031;
52; Mismatches 4; Indels
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FRAMEWORK-2.
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SHAMEWORK-1,

SHAMEWORK-2,

COMPLEMENTARITY-DETERMINING-
PRAMEWORK-3,

COMPLEMENTARITY-DETERMINING-
PRAMEWORK-3,

COMPLEMENTARITY-DETERMINING-
PRAMEWORK-4,

PRAMEWORK-4,

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BY SIMILARITY.

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                                EC46C9D259213BE4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region ABPC 22/PC 9245.
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BY SIMILARITY.
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P01662;
21-JUL-1986 (Rel. 01, Created)
                               12099 MW;
                                                                               ch 75.6%;
1 Similarity 28.2%;
22; Conservative 5
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HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; 1Gv; 1.
Immunoglobulin V region.
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111 AA;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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McKean D.J., Potter M., Hood L.E.;
Mouse immunoslobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
Biochemistry 12:760-771(1973).
BISP: PO1607; IREI.
InterPro: IPR003006; Ig_MHC.
                                                                                                                                                                                                                                  66.8%; Score 137; DB 1; Length 111; 25.6%; Pred. No. 0.01; tive 50; Mismatches 8; Indels
                                                                        COMPLEMENTARITY - DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                         12039 MW; 1E46988341858526 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-III region TEPC 124.
Mus musculus (Mouse).
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BY SIMILARITY
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InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region.
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
Matches 15; Conserv
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MEDLINE-79012520; PubMed-99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
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                                                        SEQUENCE OF 21-131.
MEDLINE-73140225; PubMed-4691517;
MCKaan D.J., Potter M., Hood L.E.;
Mouse inmunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                 KAPPA CHAIN V-III REGION MOPC 63.
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 precursors: implications on the organization and controlled
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                                                                                                                                                                                                                related mouse kappa variable regions.;
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVMSMG.
HSSP: P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SMO0406; IGy; 1.
Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 6684.
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FRAMEWORK-1
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                expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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PIR; A01938; KVMS84.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
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131 AA;
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P01670;
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ö Gaps ó 66.3%; Score 136; DB 1; Length 112; ilarity 19.2%; Pred. No. 0.013; Conservative 58; Mismatches 5; Indels 12339 MW; 7CFD328DBE8E9D71 CRC64;

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RESULT 13 KV3F\_MOUSE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                      Gray W.R., Dreyer W.J., Hood L.E.; "Mechanism of antibody synthesis: size differences between mouse
                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region MOPC 70.
                                111 AA.
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                                  PRT;
                                                                                                                                                                                                                           MEDLINE=67056897; PubMed=4162931;
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MEDLINE-79073152; PubMed=103003;
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                  STANDARD;
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38
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                                                                                                                              Mus musculus (Mouse)
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Best Local Similarity
Matches 20; Conserv
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 RESULT 14
KV3C_MOUSE
ID KV3C_MOUSE
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P01654;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 21-132.
MEDLINE-73140224; PubMed-4120629;
MCKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
24 RASZSVNWYGNSFMZWYZZKPGZPPKLLIYRASNLZSGIPARFSGSGSRTBFTLTIBPVZ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                 Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin V region; Bence-Jones protein; Signal
                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region WOPC 321 precursor.
                                                                                                                                          132 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                 expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
                                                                                                                                           PRT;
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HSSP; P01607; IREI.
InterPro; IPR033006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Biochemistry 12:749-759(1973).
                                                            84 ABDVATYFCZZSBZAPWT 101
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                               61 XXXXXXXXQQSNEDPRT 78
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                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                         Mus musculus (Mouse).
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Best Local Similarity
Matches 15; Conserv
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SEQUENCE OF 1-37.
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P01658;
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Gaps
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-i- MISCELLANBOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL..
PIR; A01930; KVMS80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 RASESVDUSGISFMNWFQQKPGQPPKLLIYAASNQGSGVPARFSGSGSGTDFSLNIHPWE
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Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 4FE7ABC9DF0FC125 CRC64;
kappa chains.";
Science 153:465-467(1967).
-! MISCELLANGOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01930; KVMS80.
HSSP; PO1799; MCP.
InterPro; IPR003066; Ig_MHC.
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25.6%; Pred. No. 0.016;
iive 50; Mismatches
                                                                                                                                                                        Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Bence-Jones protein.
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15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 2880/PC 1229.
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Search completed: August. 14, 2002, 15:23:12 Job time: 685 sec

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Compugen Ltd GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

OM protein - protein search, using sw model

August 14, 2002, 15:22:12 ; Search time 187.61 Seconds (without alignments) 71.924 Million cell updates/sec Run on:

5\_G\_6\_G\_7 205 1 KASQSVDYDGDSYMNXXXXX .....XXXXXXXXXXXXXQQSNEDPRT Perfect score:

BLOSUM62DX Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues Searched:

562222

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_19:\* Database

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\* sp\_invertebrate:\*
sp\_mammal:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_organelle:\*
sp\_phage:\* sp\_plant:\* sp\_rodent:\* sb\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_bacteriap:\*
sp\_archeap:\*

SUMMARIES

			Description	nlnosnu smu 061180;	Q920e9 mus musculu	Q96sa9 homo sapien	Q9ul77 homo sapien	Q9ul81 homo sapien	Q9u170 homo sapien	Q9u180 homo sapien	Q96jm2 homo sapien	O09004 mus musculu	Q9pmz3 campylobact	Q9fvq1 arabidopsis	Q9quq9 mus musculu	000538 homo sapien	Q9u165 homo sapien	Q9h1b6 homo sapien	Q9j176 mus musculu
7777			ID	09JF80	Q920E9	Q96SA9	Q9UL77	Q9UL81	Q9UL70	09UL80	096лм2	009004	O9PMZ3	Q9FVQ1	690060	000538	09ur65	Q9H1B6	Q9JL76
			DB	11	Ξ	4	4	4	4	4	4	Π	16	10	11	4	4	4	11
		Query	Length	103	111	107	108	107	108	114	1299	260	408	557	809	609	671	827	26
	æ	Query	Match	62.9	63.4	55.1	55.1	53.7	52.7	51.0	50.2	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.0
			Score	135	130	113	113	110	108	104.5	103	101	101	101	101	101	101	101	100.5
		Result	No.	1	7	e	4	J.	ø	7	ω,	σ	10	11	12	13	14	15	16

007324 staphylococ Q9vms2 drosophila P72503 streptococc P72572 streptococc Q9pkm5 chlamydia m	099ut0 staphylococ 09gz13 leishmania 09j174 mus musculu 025305 helicobacte 091103 lycopersico	- π O.	Q9j4x5 human immun Q97130 leishmania Q9455 caulobacter Q24593 drosophila Q9w425 drosophila Q95513 macaca fasc	Q95514 macaca fasc Q9bcy4 papio cynoc Q9sug7 arabidopsis Q9j345 human immun Q9bfq4 talpa altai Q90491 human immun Q90401 human immun
ιo.	16 099UT0 5 09GLJ3 11 09JL74 16 025305 10 09LLD3	0 0	15 Q94X5 5 Q97130 5 Q245952 5 Q24593 5 Q9W425 7 Q95513	22 20
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## ALIGNMENTS

XX STRAINBALB/C;
XX MEDLINE=20448942; PubMed=10992488;
XA MAINISE: 1. Liao. L., Cunningham M.W., Diamond B.;
XA MAINISE S., Liao. L., Cunningham M.W., Diamond B.;
XA T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
XI Infect. Immun. 68:5803-5808(2000).
XI Infect. Immun. 68:5803-5808(2000).
XI Infect. IPRO0306; Ig\_MHC.
XI INTERPOO, IPRO0306; Ig\_MHC.
XI INTERPOO, IPRO03306; Ig\_V.
XI INTERPOO, IPRO03306; Ig\_V.
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XI INTERPOORT IN IN IN IN IN IN INTERPOORT IN INTERPOORT IN INTERPOORT IN INTERPOORT IN INTERPOORT I Eukaryota:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090; 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION 103 AA. PRT; PRELIMINARY; (FRAGMENT).
Mus musculus (Mouse). [1] SEQUENCE FROM N.A. 09JI80 RESULT 09JL80 

Gaps 1 KASQSVDYDGDSYMNXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX 60 ó Query Match 65.9%; Score 135; DB 11; Length 103; Best Local Similarity 24.4%; Pred. No. 0.11; Matches 19; Conservative 52; Mismatches 7; Indels ó

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Indels

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Q920E9

RESULT **0920E9** 

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24 RASQSI----SSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQ 79
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

WINDLINE-98277139; Pubmed-9614934;
WU X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11arity 20.8%; Pred. No. 7.8; Conservative 52; Mismatches 1. Thanh
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                 09UL77;
01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
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EMBL; AF035037; AAD56273.1; -.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                108 AA.
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Best Local Similarity 20.8%; Pred. No. 7.6; Matches 15; Conservative 52; Mismatches
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InterPro; IPR003596; Ig_V.
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                                                                                                                                                                80 PEDFATYYCQOS 91
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Best Local Similarity
Matches 15; Conserv
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EMBL; AF307935; AAL09419.1; -.
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16 RASESVEYYGTSLMQWYQQKPGQPPKLLIYAASNVESGVPARFSGSGSGTDFSLNIHPVE 75
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                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLR-Lel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 63.4%; Score 130; DB 11; Length 111; Local Similarity 24.4%; Pred. No. 0.34; Hes 19; Conservative 50; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 107;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-INDICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA; 12046 MW; 1E46988AA6858526 CRC64;
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11520 MW;
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Homo sapiens (Human).
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                                                            ::::::::||| : | | | 76 EDDIAMYFCQQSRKVPWT 93
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107 AA;
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                                                                                                                                                                                                           1 KASQSVDYDGDSYMNXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXX
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Wu X., Liu B., Van der Merwe P.L., Kalls N.N., berney _{^{2}\rm{CL}}, Young D.C., "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                 Query Match 53.7%; Score 110; DB 4; Length 107; Best Local Similarity 19.4%; Pred. No. 13; Matches 14; Conservative 53; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                               B7BEDC3E41FCCA37 CRC64;
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EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; TREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                      Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD35033, AAD56269.1; -.
INTESP: POLGO7; IREI.
INTERPRO; IPRO03006; Ig_MHC.
INTERPRO; IPRO03596; Ig_N.
INTERPRO; IPRO047; ig; 1.
SMART; SMO0406; IGV; 1.
                                                                                                                                                                                                                                                                                                                           108 AA.
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108 AA; 11633 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 17.9%
Matches 14; Conservative
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SMART; SM00406; IGv; 1.
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"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro.";
DNA Res. 8:85-95(2001).
EMBL. ABOS8706; BAB47432.1; -.
SEQUENCE 1299 AA; 148675 MW; 69FFECB5868186DD CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  070E31E210D1CB01 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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EMBL; AF035034; AAD56270.1; --
HSSP; P80362; IWTL.
114 AA.
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PRT;
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MEDLINE=21245130; PubMed=11347906;
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MEDLINE=98277139; PubMed=9614934;
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InterPro; IPR003596; Ig_V.
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KIAA1803.
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Best Local Similarity 16.9%
Matches 13; Conservative
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PRELIMINARY;
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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NCBI_TaxID=197;
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                                            1 KASQSVDYDGDSYMNXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXX 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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A Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
A Gedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
I'The germinal centre kinase gene and a novel CDC25-like gene are
I located in the vicinity of the PYGM gene on 11q13.";
Hum. Genet. 100:611-619(1997).
I-- SIMILARITY: TO OTHER EP-HAND CALCIUM BINDING PROTEINS.
REMBL: 712339; CAA73008.1; -.
HSSP; P28867; 1PTQ.
RGD; MGI:1333849; Rasgrp2.
R InterPro; IPR002219; DAG_PE-bind.
R InterPro; IPR002048; EP-hand.
R PÉan; PF00036; efhand; 2.
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  Length 1299;
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                       11; Indels
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                                                                                                                                                                                               Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN CJ1306C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.3%; Score 101; DB 11;
12.9%; Pred. No. 4.8e+02;
tive 55; Mismatches 6;
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; Pred. No. 9.7e+03;
51; Mismatches 11;
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01-JUL-1997 (TrEMBLrel. 04, Last sequenc
01-DEC-2001 (TrEMBLrel. 19, Last annotat
F25B3.3 KINASE LIKE PROTEIN (FRAGMENT).
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PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
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 50.2%;
17.3%;
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1229 HGMALNDTKQVSREE 1243
                       13; Conservative
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                                                                                      61 XXXXXXXXQQSNED 75
            Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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SEQUENCE
  Query Match
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                       Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 20150912; Pubmed=10688204;

MEDLINE=20150912; Pubmed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Mitchead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences.";

In Rutre 403:665-668(2000)

In Rutre 403:665-688(2001)

IN Rypothetical protein; Complete proteome,

SEQUENCE 408 AA, 47256 MM; DD0D034E75EF7C22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. STRAIN=CV. COLUMBIA;
A. Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
A. Maitl R., Ronning C.M., Roo H., Fujii C.Y., Utterback T.R.,
B. Maristed M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
T. "Arabidopsis thaliana chromosome 1 BAC F27K7 genomic sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
I. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
R. REMBL; AC084414; AAG29744.1;
R. RITERPO; IPR000504; RRM.
R. RPROSITE; PS50102; RRM; 2.
R. PROSITE; PS50102; RRM; 2.
R. PROSITE; PS50102; RRM; 2.
R. ROSITE; PS50102; RRM RNP-1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 KSKDINGDMYMQCDHFFVSCFLKTHWTRKENSPYFFNNENYFIRTLLNKDHLILQSQKNK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
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Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUMI PROTEIN, PUTATIVE.
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Matches 12; Conservative
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Best Local Similarity 17.3'
Matches 13; Conservative
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496 GFVHNFQESN 505

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Ganglia
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                                                                                                                                                                                                                                                                                                                                          Kawasaki H., Springett G.M., Toki S., Canales J.J., Blumenstiel J.P., Chen B.J., Bany I.A., McChizuki N., Ashbacher A., Matsuda M., Housman D.E., Graybiel A.M., "A Novel Rap Guanine Nucleotide Exchange Factor Enriched in the Basal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CALCIUM-AND DIACYLGLYCEROL-REGULATED GUANINE NUCLEOTIDE EXCHANGE
FACTOR I.
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                                                                                                                                                                                                                                                                                                                                                                        Kawasak1 H., Housman D.E., Graybiel A.M.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         608 AA; 69294 MW; DC717794CE12C2D1 CRC64;
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                                                         608 AA.
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INTERPO; IPRO02219; DAG PE-bind.
INTERPO; IPRO02219; DAG PE-bind.
INTERPO; IPRO0189; EF-band.
INTERPO; IPRO01895; RASGRE_CDC25.
Pfam; PF000130; DAG_PE-bind; I.
Pfam; PF000130; DAG_PE-bind; I.
SMART; SM00109; C1; I.
SMART; SM00109; C1; I.
SMART; SM00147; RASGEF; I.
PROSITE; PS00047; DAG_PE_BIND_DOM_I; I.
PROSITE; PS000479; DAG_PE_BIND_DOM_I; I.
PROSITE; PS000479; DAG_PE_BIND_DOM_I; I.
PROSITE; PS000419; DAG_PE_BIND_DOM_I; I.
PROSITE; PS000419; DAG_PE_BIND_DOM_I; I.
PROSITE; PS000419; DAG_PE_BIND_DOM_I; I.
PROSITE; PS000419; DAG_PE_BIND_DOM_I; I.
                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
                                                         PRT;
                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-99007305; PubMed=9789079;
242 SKKSSSDESSESED 256
                                                         PRELIMINARY;
                                                                                                                               RASGRP2 OR CALDAG-GEFI, Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                    RESULT 12
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SEQUENCE FROM N.A.
MEDLINES-99007305; PubMed=9789079;
Kawasaki H., Springett G.M., Toki S., Canales J.J., Harlan P.,
Rawasaki H., Springett G.M., Toki S., Mochizuki N., Ashbacher A.,
Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N., Ashbacher A.,
Matsuda M., Housman D.E., Graybiel A.M.;
"A Rap guanine nucleotide exchange factor enriched highly in the basal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawasaki H., Springett G.M., Toki S., Canales J.J., Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N., Ashbacher A., Matsuda M., Housman D.E., Graybiel A.M.;
"A Novel Rap Guanine Nucleotide Exchange Factor Enriched in the Basal
                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-28001089; PubMed-9341881;
Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
"The germinal center Kinase gene and a novel CDC25-like gene are
located in the vicinity of the PYGM gene on 11q13.";
Hum. Genet. 100:611-619(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawasaki H., Housman D.E., Graybiel A.M.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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to the EMBL/GenBank/DDBJ databases
                                                                                     Last sequence update)
Last annotation update)
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609 AA.
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InterPro: IPR002048; EF-hand.
InterPro: IPR002048; EF-hand.
InterPro: IPR001895; RASGEF.
InterPro: IPR001895; RASGEF.
Pfam: PF000130; DAG_PE-bind; 1.
Pfam: PF00036; efhand; 2.
Pfam: PF00017; RASGEF; 1.
SMART; SM00109; CI; 1.
SMART; SM00109; CI; 1.
SMART; SM00147; RASGEF; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_I; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_I; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
                                                          Created)
PRT;
                                                    01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                            F25B3.3 KINASE LIKE PROTEIN
PRELIMINARY;
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Submitted (FEB-1999)
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RX PEQUENCE FROM N.A.

RA ADDIDINE-20493616; PubMed=10918068;

RA ADJUENCE-Smith J., Silins G., Gartside M., Grimmond S., Etheridge M., Apolloni A., Hayward N., Hancock J.F.;

RA Apolloni A., Hayward N., Hancock J.F.;

RT "Characterization of RasGR2D, a Plasma Membrane-targeted, Dual RT "Characterization of RasGR2D, a Plasma Membrane-targeted, Dual RT "Specificity RasRap Exchange Factor.";

LJ Biol. Chem. 275:32260-32267(2000).

CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.

DR HSSP; P28867; 1PTQ.

DR HSSP; P28867; 1PTQ.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR000651; RasGERN.

DR Fam; PF000130; DAG_PE-bind; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00109; DAG_PE_BIND_DOM_1; 1.

DR SMART; SM00109; DAG_PE_BIND_DOM_1; 1.

DR PROSITE; PS00479; DAG_PE_HIND_DOM_2; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
                                                                                                                     Gaps
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
                                                 49.3%; Score 101; DB 4; Length 609; 12.9%; Pred. No. 2.9e+03; ive 55; Mismatches 6; Indels
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Calcium-binding; Phorbol-ester binding.
SEQUENCE 609 AA; 69248 MW; 8B1321F864D24BC7 CRC64;
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                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GUANINE EXCHANGE FACTOR MG7 ISOFORM 1.
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49.3%; Score 101; DB 4;
Best Local Similarity 12.9%; Pred. No. 3.5e+03;
Matches 9; Conservative 55; Mismatches 6;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                      Query Match
Best Local Similarity 12.9*
Conservative
Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                       496 GEVHNFQESN 505
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                                                                                                                                                        64 XXXXXXQQSN 73
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SEQUENCE 671 1
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ID Q9H1B6
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MEDLINE-20553456; Pubmed-11099377;
Goetting C., Kuhn J., Zahn R., Brinkmann T., Kleesiek K.;
Molecular cloning and expression of human UDP-D-xylose:proteoglycan core protein beta-D-xylosyltransferase and its first isoform XT-II.";
J. Mol. Biol. 304:517-528(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "First isolation of human UDP-D-xylose:proteoglycan core protein beta-D-xylosyltransferase secreted from cultured JAR choriocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KASQSVDYDGDS--YMNXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Kuhn J., Goetting C., Schnoelzer M., Kempf T., Brinkmann T.,
Kleesiek K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 827;
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01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
XYLOSYLTRANSFERASE I (EC 2.4.2.26) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 49.3%; Score 101; DB 4; Lv Best Local Similarity 17.3%; Pred. No. 5.5e+03; Matches 13; Conservative 53; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: August 14, 2002, 15:22:14 Job time: 682 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ277441; CAC16787.1; -. Transferase; Glycosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 0:0-0(0)
                                                                                                                                                        Homo sapiens (Human)
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SEQUENCE 827 AA;
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August 14, 2002, 15:15:34; Search time 230.21 Seconds (without alignments) 114.832 Million cell updates/sec
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1237
1 METDIILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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5. SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
6. SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:\*
7. SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas
SUMMARIES	ID	AAW90930	AAW90932	AAW90931	AAW83034	AAB14777	AAW90927	AAW83031	AAB14772	AAW90922	AAW83032	AAB14773
	DB	21	21	21	19	21	21	19	21	21	19	21
	Query Match Length DB	238	238	238	238	238	238	238	238	238	238	238
ф	Query	100.0	66.66	66.7	94.8	94.8	94.8	94.4	94.4	94.4	93.4	93.4
	Score	1237	1236	1233	1173	1173	1173	1168	1168	1168	1155	1155
	Result No.	-	7	m	4	S	9	7	80	6	10	11

98JP-0276882

30-SEP-1998;

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(SANY ) SANKYO CO LTD.

13	1155	93.4	238	19	AAW83035	anti-Fa humanise
4.4	1154	93.3	238	27	AAB14778	Humanised anti-Fas
	1153	93.2	238	136	AAW83033	nre/A humanis
	1153	93.2	238	21	AAB14774	
	1153	93.2	238	21	AAW90924	
	1112	6.68	218	18	AAW13563	Humanised anti-L-s
	1100	88.9	218	20	AAW95658	Mus musculus anti-
	1100	6.88	218	21	AAY85200	Light chain amino
	1100	88.9	218	22	AAB76947	Full variable ligh
	1093	88.4	218	14	AAR33312	Humanised MaE11 Ve
	1077	87.1	218	20	AAY50030	Human E27 anti-1gE
	1077	87.1	218	20	AAW95660	Mus musculus anti-
	1077	87.1	218	20	AAW95662	Mus musculus anti-
	1077	87.1	218	21	AAB07472	Amino acid sequenc
 80	1077	87.1	218	22	AAB74211	E27 anti-IgE antib
	1074	ė.	218	20	AAW95669	Mus musculus anti-
	1074	86.8	218	20	AAW95664	Mus musculus anti-
	1074	ġ.	218	22	AAB47087	Anti-IgE antibody,
	1074	9	218	22	AAB76949	Full length light
	1074	86.8	218	22	AAB76951	Full length light
	1074	9	218	22	AAB76953	Variable light cha
	1074	٠,	218	22	AAB76958	Variable light cha
-	053.5	'n.	237	21	AAY96298	Human IGFAM-10 imm
	1049.5	4.	237	21	AAY96289	Human IGFAM-1 immu
	1047.5	84.7	241	22	AAB82912	Human immune respo
	1045.5	84.5	234	14	AAR38162	Sequence of the ka
	1044	84.4	240	20	AAY50161	Human reshaped F19
Н	041.5	84.2	237	21	AAY96301	Human IGFAM-13 imm
	1040	84.1	234	18	AAW11638	Human anti-RSV mon
	1027	83.0	240	22	AAG63665	Amino acid sequenc
	1023	82.7	236	16	AAR77614	Humanised 5G1.1 VL
10	1022.5	82.7	233	14	AAR30777	pH52-9.0 humanised

## ALIGNMENTS

RESULT AAW9093	RESULT I	
e X	AAW90930 stand	AAW90930 standard; Protein; 238 AA.
AC	AAW90930;	
×		
E X	08-AUG-2000 (first entry)	first entry)
DE	Humanised ant	Humanised anti-Fas designed light chain Leu 1 protein.
×		
ΚW	Fas; antibody,	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
ΚW	anti-allergic,	anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
ΚW	dermatologica.	dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
ΚW	nephrotropic;	nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
ΚW	hepatotropic;	hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
ΚW	Hashimoto dise	Hashimoto disease; rheumatoid arthritis; graft versus host disease;
ΚW	Sjorgen's sync	rome; anemia; Addison's disease; scleroderma; sterility;
ΚM	Goodpasture sy	<pre>Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;</pre>
ΚW	multiple scle	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
ΚW	insulin depend	ent diabetes mellitus; arteriosclerosis; myocarditis;
ΚW	cardiomyopathy	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX		
SO	Synthetic.	
××		
ΡN	EP990663-A2.	
XX		
PD	05-APR-2000.	
XX		
ΡF	29-SEP-1999;	99EP-0307711.
X		
PR	30-SEP-1998;	98JP-0276881.

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Eas anotates ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, darmatological, immunosupressive, thyromimetic, antiviral, immunomodulatory, darmatological, antidifertility, neuroprotective, antiarteriosclerofic, cardiant and hepatropic activity. (I) induce antiarteriosclerofic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding (I) are used to treat and/or prevent capoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive canemia, stythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, slorgem's syndrome, pernicious or hypoplastic versus host disease, slorgem's syndrome, goodpasture syndrome, Codisease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection, (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic multine disease models. (I) act on the active site of Fas, i.e. they minic multine disease models. (I) act on the active site of Fas, i.e. they minic a human anti-murine antibody light channomative lessignated Leu i and have reduced risk a humanised anti-manised anti-manised anti-manised anti-manised anti-manised anti-manised anti-manised anti-manised anti-manised 
                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                  Takahashi T;
                                  Tamaki I,
                            Nakahara K,
                                                                                                                                                                                                                                                                                                  263pp; English.
                                  Haruyama H,
                                                                                                                                                                                                                                                                                                  Claim 3; Page 156-157;
                                                                                    WPI; 2000-258930/23.
                                                                                                                   N-PSDB; AAA11631
                                  Serizawa N,
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238 AA; Sequence

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                                                                                                                   QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                 121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                          1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                      181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
   Length 238;
                               Indels
100.0%; Score 1237; DB 21;
100.0%; Pred. No. 6.7e-62;
iive 0; Mismatches 0; I
               Best Local Similarity 100.
Matches 238; Conservative
   Query Match
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Humanised anti-Fas designed light chain Leu 3 protein. AAW90932 standard; Protein; 238 AA. (first entry) 08-AUG-2000 AAW90932; RESULT AAW90932 BXAXAXB

anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic, antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Godpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. antidiabetic; antibody; human; anti-inflammatory; anti-anemic;

EP990663-A2 Synthetic.

05-APR-2000

99EP-0307711. 29-SEP-1999; 98JP-0276881. 30-SEP-1998;

98JP-0276882. 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Haruyama H, Nakahara K, Tamaki I, Takahashi T; Serizawa N,

WPI; 2000-258930/23. N-PSDB: AAA11633 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 3; Page 161-162; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

capoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

anti-innemic, antidiabetic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antirheumatic, nephrotropic, antilnfertility, neuroprotective,

cantinheumatic, nephrotropic, antilnfertility, neuroprotective,

capoptosis by binding to cell surface Fas or inhibit it by competitive

capoptosis by binding to cell surface Fas or inhibit it by competities,

canedia, Addison's disease, scleroderma, goodpasture syndrome, Crohn's

canedia, Addison's disease, stleroderma, coodpasture syndrome, Crohn's

canedia, Addison's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

calcomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

Cardiomyopathy, glomerulonephritis, series of Fas, i.e. they minic

calls. They bind to both hu 

Sequence

ö Gaps ő Length 238; Indels Score 1236; DB 21; Pred. No. 7.6e-62; 1; Mismatches 0; 99.98; 99.68; Query Match Best Local Similarity 99.6 Matches 237; Conservative

1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60

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AAW83034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; antialogy; darti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-fas; nephrotroptc; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-diabetic, anti-allergic, anti-arthritic, anti-viral, immunosuphatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity, (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized anti-Fas'antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                    TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                         QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                             GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                             Takahashi T;
                                                                                                                                                                                                                                                                                                                       Humanised anti-Fas designed light chain Leu 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakahara K, Tamaki I,
                                                                                                                                                                                                                                        AAW90931 standard; Protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-0307711
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N-PSDB; AAA11632.
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                                                                                                                                                                                                                                                                                            08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serizawa N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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disease, autoimmune hemolytic anemaia, sociality, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocardinis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody light chain construct designated Leu 2 which is described in the method of the invention.
diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematcosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OOKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCOOSNEDPR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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Sjogren syndrome; pernicious anaemia; Addison's disease;
scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%; Score 1233; DB 21; Length 238; 99.6%; Pred. No. 1.1e-61;
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apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Fas humanised antibody HFE7A light chain PDHH type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1223,
Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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21..238
/label= Mat_protein
21..131
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/label= Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.6
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

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chain of murine anti-human Sequence of the PDHH type numanised light.

Chain of murine anti-human Sequence (see AAW83042) entailed making

EDE, PATA, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K

munic acid substitutions; these residues are conserved in the

human light chain (kappa chain). Host cell Escherichia coli

phSHH5 SANK 7039B harbors plasmid pHSHH5 carrying a fusion

fragment of the humanised PDHH type HFSH5 alight chain and DNA

encoding the region of human immunoglobulin kappa chain, and is

deposited as FERW BP-6274 (claimed). The invention provides

methods for producing humanised antibodies by culturing host

cells. Humanised versions of HFBTA (see AAW83011-37). like native

HFBTA, are capable of inducing apoptosis in abnormal cells

cells. The humanised antibodies are used to evaluate, in animal

cells. The humanised antibodies are used to evaluate, in animal

models, treatments of diseases that involve Fas/Fas ligand

interactions, and also to treat such diseases, including autoimmune

disease (e.g. systemic lupus erythematosus, Hashimoto's disease,

craft versus host disease, scleroderma, Goodpasture syndrome, Crohn's

sterility. Masterband arravis multinite autoimme haemolytic anaemia,

sterility. Masterband arravis multinite autoimmenent expericious anaemia,

sterility. Masterband arravis multinite syndrome, crohn's

sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thromobenia purpura and insulin-dependent diabetes), allergies, attopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, 'allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the PDHH type humanised light
                                                                                                                                                                                                                                                                                                                                                                                                                                         in O, Kimihisa I;
Tohru T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 218; 292pp; English.
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S, Shin Y,
                                                                                                                                       113..121
/label= CDR_L3
/note= "claim 9"
                 'label - Constant
                                                                                                                          /note= "claim 9"
                                                                      /note- "claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocarditis, hepatitis and AIDS
                                                                                      74..80
/label- CDR_L2
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/label- CDR_L1
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97JP-0082953.
97JP-0169088.
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O, Nobufusa
                                                                                                                                                                                                                                                                                                                                                                                                      SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                       30-MAR-1998;
                                                                                                                                                                                                                                                                                                                             08-OCT-1997;
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25-JUN-1997;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, attendocatesis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AABI4772-B14774 and AABI4777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agent for the diseases caused by an abnormality
181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                        the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised anti-Fas antibody light chain, SEQ ID NO:107.
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                                                                                                                                                                                                                                                                                                                                                                            AAB14777 standard; Protein; 238
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238 AA;

Sequence

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Gaps

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94.8%; Score 1173; DB 19; Length 238; 92.9%; Pred. No. 2.4e-58; Live 10; Mismatches 7; Indels 0

Local Similarity 92.9 ses 221; Conservative

Matches

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Query Match

1 METDTILLWWVLLLWWPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60

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Homo sapiens.
Synthetic.
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                          QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                     TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                Gaps
                                                             1 METDTILLWVLLLWWPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                             GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                 antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                Indels
Pred. No. 2.4e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised HFE7A designed light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 141-142; 263pp; English.
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 92.98; Fil
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98JP-0276882.
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                al Similarity 92.9
221; Conservative
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                Best Local
Matches 22
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.8%; Score 1173; DB 21
92.9%; Pred. No. 2.4e-58;
iive 10; Mismatches 7
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 94.89
Best Local Similarity 92.99
Matches 221; Conservative
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chain of murine anti-human Fargence (see AAM83042) entailed making P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSGHH7 SANK 73497 harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised HT type HFE7A light chain and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A carrying host cells. Humanised versions of HFE7A carrying host cells. Humanised versions of HFE7A carrying host cells. The humanised versions of the captosis in abnormal cells expressing Fas, and of inhibiting apoptosis in normal cells. The humanised antibodies care used to evaluate, in animal models, treatments of diseases that involve FasyFas ligand interactions, and also to treat such classases, including autoimmune disease (e.g. systemic lupus certifications). Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin'dependent diabetees), allergies, attopy, arteriosclerosis, anyocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the HH type humanised light
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Shin Y, Tohru T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 199-199; 292pp; English.
21..238
/label= Mat_protein
                                                   /label= Variable
                                                                                     /label- Constant
                                                                                                                                     note= "claim 9"
                                                                                                                                                                                           /note= "claim 9"
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                                                                                                                                                       74..80
/label= CDR_L2
                                                                                                                                                                                                         113..121
/label- CDR_L3
                                                                                                       44..58
/label= CDR_L1
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97JP-0169088
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25-JUN-1997;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HEFTA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; carditomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
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                                                                                                                                                                                                                                                QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                       121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDXDGDSYMNWY
                                                                                                                                 1 metdtillwvlllwvpgstgdivltqspgtlslspgeratlsckasqsvdydgdsymnwy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-Fas antibody light chain, SEQ ID NO:50.
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Chimeric - Homo sapiens.
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238 AA;

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Gaps

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Length 238; Indels

3; Up. 4.6e-58; 8;

94.4%; Score 1168; DB 19; 1larity 92.4%; Pred. No. 4.6e-58; Conservative 10; Mismatches 8;

Similarity

Local Simi hes 220;

Best Loca Matches

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                           QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                         121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                 Gaps
                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                       GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised anti-Fas antibody HFE7A light chain HH type protein.
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Length 238;
                               Indels
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DB 21;
94.4%; Score 1168; DB 21
92.4%; Pred. No. 4.6e-58;
                              10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells with abnormal Fas-Fas ligand systems
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                               Conservative
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Query Match
                Local
                              Matches
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cc Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antirhemmatic, nephrotropic, antilhertility, neuroprotective, antiarteriosclerotic, antiminertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, antiple sclerosis, basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomypathy, glomerulonephitis, hepatitis (fulminant, chronic, viral (8), C or D) or alcoholic), and transplant rejection. (1) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, 1.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody response. This sequence represents the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis; HEETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFE7a; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-Fas humanised antibody HFE7A light chain HM type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%; Score 1168; DB 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.4%; Pred. No. 4.6e
live 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW83032 standard; Protein; 238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sim
Matches 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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/label= Sig_peptide
21..238
Location/Qualifiers
                  /label- Mat_protein
                                                                                                                                                                                                 Claim 21; Page 200; 292pp; English.
                       21..131
/label= Variable
                                     /label= Constant
                                                   'note= "claim 9"
                                                                'note= "claim 9"
                                                                              /note- "claim 9"
                                                                    113..121
/label= CDR_L3
                                          44..58
/label= CDR_L1
                                                        74..80
/label= CDR_L2
                                                                                                                  97JP-0276064.
97JP-0082953.
97JP-0169088.
                                                                                                          98AU-0059701
                                132..238
                                                                                                                                     (SANY ) SANKYO CO LID.
                                                                                                                                                            WPI; 1998-543440/47.
                                                                                                                                                                 N-PSDB; AAV70075
                                                                                                                        01-APR-1997;
25-JUN-1997;
                                                                                                          30-MAR-1998;
                                                                                                                   08-OCT-1997;
                                                                                       AU9859701-A
                                                                                                 08-OCT-1998
    Peptide
             Protein
                       Region
                                Region
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This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coll p46GHM17 SANK 73597 harbors plasmid pHSGHM17 carrying a fusion fragment of the humanised and immunoglobulin kappa chain, and is encoding the region of human immunoglobulin kappa chain, and is emptoded so FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW8301-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lugus expthematosus, Hashimoto's disease, condessing actioned arthritis, autoimmune settlity, myasthenia gravis, multiple sclerosis, Basedow's disease, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, hypoplastic anaemia New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I; Masahiko O, Nobufusa S, Shin Y, Tohru T; 238 AA; Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, arteriosclerosis, myocarditis, cardiomyopathy glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                         121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                    QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                 Gaps
                                                                                            1 METDIILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNMY 60
                                                                                                                                                                                                                                                                                                                            181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                     ö
Length 238;
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                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody light chain, SEQ ID NO:52.
                                 . 0,
93.4%; Score 1155; DB 19;
                 Pred. No. 2.4e-57
                                     11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB14773 standard; Protein; 238 AA.
                 91.6%;
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                                   Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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N-PSDB; AAA72125.
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-Fas antibody
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 Query Match
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                                                                    0;
                                                                                                                                                                                                                                                                                                                                                               Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; mysthenia gravis; multiple sclerosis; Basedow's disease; thermbopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                        121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                     Gaps
                                                                                       1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                   GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory or autoimmune disease, induces apoptosis selectively cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                               Humanised anti-Fas antibody HFE7A light chain HM type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakahara K, Tamaki I, Takahashi T;
                                                Length 238;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for treating or
                                                 ; LL
2.4e-57;
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example reference 14; Page 117-118; 263pp; English.
                                                                   11; Mismatches
                                                93.4%; Score 1155;
                                                            Pred. No.
                                                                                                                                                                                                                                                                                   AAW90923 standard; Protein; 238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0276881.
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                                                            91.68;
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haruyama H,
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-258930/23.
                                                          Similarity
                    238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA11563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                           08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serizawa N,
                                                            Best Local Sim
Matches 218;
antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                        AAW90923;
                    Sequence
                                                Query Match
                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                          AAW90923
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molecule (1) that, induces apoptosis in cells with an abnormal Pas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antifital
immunomodulatory, dermatological, immunosuperssive, thyromimetic,
antistemmatic, nephrotropic, antinifertility, neuroprotective,
antistemmatic, nephrotropic, antinifertility, neuroprotective,
antistemmatic, antinifertility, neuroprotective,
antistemmatic, nephrotropic, antinifertility, neuroprotective,
antistemmatic, sandant and hepatropic activity. (I) induce
antistemmatic, sandant and hepatropic activity. (I) induce
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
clusus systemmatosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Slorgen's syndrome, Goodpasture syndrome, Crohn's
antiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, mycarditis,
cardiomyopethy, glomenla, pepaticis, fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFETA light chain HM type which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombopenia purpura; insulin-dependent diabetes; allergy; actopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1155; DB 21
Pred. No. 2.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
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Best Local S
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(SANY ) SANKYO CO LTD.
                                                                                       WPI; 1998-543440/47.
                                                                                         N-PSDB; AAV70078
Homo sapiens.
Synthetic.
                                                                  08-OCT-1997;
                                                             30-MAR-1998;
                                                                    01-APR-1997;
25-JUN-1997;
                                                   AU9859701-A
                                                        08-OCT-1998
         Peptide
              Protein
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93.3%; 91.6%; 99JP-0278301. 98JP-0276883. (first entry) Query Match 93.3 Best Local Similarity 91.6 Matches 218; Conservative Chimeric - Mus musculus. Chimeric - Homo sapiens. (SANY ) SANKYO CO LID. WPI; 2000-485645/43. 238 AA; anti-Fas antibody N-PSDB; AAA72177 JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 24 - NOV - 2000 20-JUN-2000 Sequence AAB14778; 61 AAB14778 S g g 셤 δy g ò ŏ chain of murino acid sequence (see AAW83042) entailised right.

Chain of murine anti-human Feas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell Escherichia coli pHSHM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the human immunoglobulin kappa chain, and is deposited as FERM BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells capressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Soleroderma, Goodpasture syndrome, pernicious anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, atopy, atteriosclerosis, mycoarditis, cardiomypathy, glomerular nephitis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed). New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS This is the amino acid sequence of the PDHM type humanised light Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I; Masahiko O, Nobufusa S, Shin Y, Tohru T; Claim 21; Page 220-221; 292pp; English. /label- Sig\_peptide label - Mat\_protein ocation/Qualifiers /113..121 /label= CDR\_L3 /note= "claim 9" 1..131 | Tabel = Variable 'label - Constant 'note= "claim 9" /label- CDR\_L2 /note- "claim 9" 14..58 /label- CDR\_L1 97JP-0276064. 98AU-0059701 97JP-0082953 97JP-0169088 132..238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                        Gaps
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Length 238;
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                                                                                    Indels
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        DB 19;
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        Score 1154; DB 19
Pred. No. 2.7e-57;
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Example reference 21; Page 144-145; 263pp; English.

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glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and Organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas antibodies.
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inflammatory or autoimmune disease, induces apoptosis selectively in
cells with abnormal Fas-Fas ligand systems
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                                                                                                                        DB 21; Length 238;
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                                                                                                                                                    Indels
                                                                                                                      93.3%; Score 1154; DB 21;
91.6%; Pred. No. 2.7e-57;
1ve 11; Mismatches 9;
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98JP-0276882.
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Matches 218; Conservative
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                                                                                                                                                                                                                      molecule (1) that, induces approsis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-alergic, anti-arthritic, antiviral, immunomodulatory, dermatchlogical, immunosuppressive, thyromimetic, antistrending the immunomodulatory dermatchlogical, immunosuppressive, thyromimetic, antistrending to antistrentiate, antinifertility, neuroprotective, antistrending to cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, permitties, graft versus host disease, Sjorgen's syndrome, permitaliculus or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
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                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like
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91.6%; Pred. No. 2.7e-57
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11; Mismatches
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Job time: 832 sec
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     RESULT
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(without alignments)
70.141 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep:*
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Compugen Ltd.
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US-08-466-163B-9
US-09-282-505-1
US-09-054-255-1
US-08-887-352B-15
US-08-887-352B-17
US-08-887-352B-17
US-09-109-207C-17
US-09-109-207C-17
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US-09-296-005-17
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PCT-US93-07832-39
US-07-934-373C-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-109-207C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-07832-25
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                           GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               protein search, using sw model
                                                                                                                                                                                    August 14, 2002, 15:17:03
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Maximum |
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APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ ?
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Pred. No. 1.6e-87;
US-08-788-800-11

US-08-437-642B-40

US-09-097-309-2

US-09-097-171A-2

PCT-US93-0783Z-40

US-09-097-171A-10

US-09-097-171B-2

US-09-422-712B-2

US-09-422-712B-2

US-09-027-449-62

US-09-1027-449-51

US-08-107-444A-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-72

US-09-026-985-72

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US-09-026-985-72
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 965
FILING DATE: 19-SEP-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein PCT-US96-13152-2
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: U.S.A.
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CLASSIFICATION:
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121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                             81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                           141 IFPPSDEQLKSGTASYVCLLNNFYPREAKVOWKVDNALQSGNSQESYTEQDSKDSTYSLS 200
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                                    21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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   2; Indels
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Pred. No. 1.7e-86;
                                                                                                                                                                                                                                                                                  181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                                                                                                             201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   2; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SYODOMA, CTALG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
TELECPHONE: 650/255-1489
TELEPHONE: 650/255-1489
TELEPHONE: 650/255-1489
TELEPHONE: 650/255-1489
TELEPHONE: GSO/255-1489
TELEPHONE: GSO/352-1881
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08887352B Patent No. 5994511
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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97.7%;
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Matches 214; Conservative
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US-08-887-352B-13
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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Pred. No. 1.7e-86;
2; Mismatches 3;
181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVERTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFRAX: 650/0623-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                      Sequence 9, Application US/08466151
Patent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07/744768
                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                             Genentech, Inc
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Best Local Similarity 97.7%;
Matches 213; Conservative 2
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FILING DATE: 14-AGG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CTAIG G.
REGISTRATION NUMBER: 39,(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                     US-08-466-151-9
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                                                                                                                                                                                                                                                                                                                          IFPPSDEQLKSGTASYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                 Gaps
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                                                                                                                                                                     21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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                                                                                           Length 218;
                     from MAE11
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                                                                                                                               Indels
                                                                                           Score 1100; DB 4;
Pred. No. 1.7e-86;
2; Mismatches 3;
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Best Local Similarity 97.7%; Pred. No. 1.7e-86;
Matches 213; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                    201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived
US-09-296-005-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR RILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                        181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                           Query Match
Best Local Similarity 97.7%;
Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-466-163B-9
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CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER RILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
                                                                                                                                                                                                     Sequence 13, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
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IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
               141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.9%; Score 1100; DB 4; Length 218; 97.7%; Pred. No. 1.7e-86; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Artificial
LOCATION: 1-218
CHER INFORMATION: Light chain sequence derived from MAE11
MS-09-108-207C-13
                                                                   STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09296005 Patent No. 6290957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similaria,
Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 218
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                           81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                               61 GVPSRFSGSGGGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
                                                                                                                                                    121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997

CLASSIFICATION: 530
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Pred. No. 2.8e-84;
                                                                                                                                                                                                            STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08887352B Patent No. 5994511 GENERAL INFORMATION:
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NAME: SVODODA, Craig G.
REGIERATION UNDRER: 39,044
REFERENCE/DOCKET UNDRER: P112:
TELECOMMUNICATION INFORMATION:
TELEFONE: 650/252-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
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STATE: California
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Best Local Similarity 95.4%;
Matches 208; Conservative
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Amino Acid
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Pred. No. 1.6e-84;
4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Sequence is completely synthesized ; Patent No. 6194551 US-09-282-505-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: E27 anti-1gE antibody light chain US-09-054-255-1
181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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Patent No. 6242195
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogle et al.
TILLE OF INVENTION: POLYPEPTIDE VARIANTS
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
SEQ ID NO 1
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
                                                                                                    Sequence 1, Application US/09282505A Patent No. 6194551
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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95.9%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 95.9 Matches 209; Conservative
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                                                            RESULT 7
US-09-282-505-1
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Pred. No. 2.8e-84;
5; Mismatches 5;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/AMS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PITELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
                     ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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Best Local Similarity 95.4%;
Matches 208; Conservative
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  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino Acid
                                                                                                        COUNTRY: US.
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                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTYON: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTYON: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
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Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1074; DB 2;
Pred. No. 2.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELEPHONE: 650/225-1489
TELEPHONE: 650/255-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08887352B Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonar TITLE OF INVENTION: Improved Anti-TITLE OF INVENTION: Improving Poly
                                                                                                             Sequence 17, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.8%;
95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 218 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.8
Best Local Similarity 95.4
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linear
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-887-352B-17
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US-08-887-352B-19
                                                                  RESULT 10
US-08-887-352B-17
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Gaps

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Sequence 17, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
FILE REFERENCE: P1123R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICAMT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION:
FILE REFERENCE: PILIZRI
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
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               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17
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86.8%; Score 1074; DB 4;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5;
                                                                                                                                                                                             STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                  201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILING DATE: 1997-07-03
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SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial
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US-09-109-207C-17
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAAPSVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       86.8%; Score 1074; DB 2;
95.4%; Pred. No. 2.8e-84;
1ive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1074; DB 4;
Pred. No. 2.8e-84;
5; Mismatches 5;
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...ек: US/08/887,352B
03-Jul-1997
N: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09109207C Patent No. 6172213 GENERAL INFORMATION:
                                                   FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G
REGISTRATION NUMBER: 39,044
                                                                                                                                                           REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
95.4%;
                                                                                                                                                                                                                                                                                            LENGTH: 218 amino acids TYPE: Amino Acid
        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: Linear
US-08-887-352B-24
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                            Gaps
                                                                                                                     ) ORGANISM: Artificial
FEATURE:
NAME/RE: Artificial
LOCATION: 1-218
OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19
                                                                                                     ;
0
                                                                               Length 218;
                                                                              Score 1074; DB 4; Length 2
Pred. No. 2.8e-84;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                      Query Match 86.8%;
Best Local Similarity 95.4%;
Matches 208; Conservative
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Search completed: August 14, 2002, 15:17:03 Job time: 686 sec

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August 14, 2002, 15:18:58; Search time 108.64 Seconds (without alignments) 210.505 Million cell updates/sec
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1237
1 METDIILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                     283138 segs, 96089334 residues
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description				chain	kappa chain		kappa chain	kappa chain	kappa chain	⊆	kappa ch	kappa chain	kappa chain		kappa chain			Ig kappa chain - m		kappa			kappa chain	-kappa protei	kappa		g kappa chain	g lambda	Ig kappa chain C r
SUMMARIES	ΩI	JE0242	JE0244	JE0243	A23746	JE0241	S06084	S14237	S68241	S33161	JC5810	S01320	A31790	A56169	S37484	PC4203	S38865	S25058	S52028	S68212	S42772	S16112	JL0029	A20969	S52059	PT0219	S29593	PH1226	A49633	КЗНО
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	Length	215	215	215	215	216	24(	234	218	23(	218	234	22(	21(	225	216	215	235	215	214	217	218	225	225	135	178	197	131	238	106
dF	Query Match	76.4	74.9	73.0	71.6	70.9	65.4	61.1	60.5	60.5	60.4	58.9	58.7	58.0	57.9	57.4	57.1	57.1	56.9	56.3	56.1	55.6	54.7	49.6	49.2	49.2	47.1	46.8	46.0	44.3
	Score	945.5	926.5	903.5	885.5	877	808	756	749	748.5	747	729	726	718	716.5	709.5	706.5	706.5	703.5	697	693.5	687.5	676.5	613.5	608.5	608	582.5	579	568.5	548
	Result No.		7	ю	4	ស	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

kappa chain	kappa chain	kappa chain	kappa chain	light chain	kappa chain	~	kappa chain	kappa chain	kappa chain	light chain	chain				
PL0106	KVMSM6	S40331	S40367	S29577	KVMS32	A49134	A37927	S40365	S26653	S20631	S40370	PN0446	S40334	S55027	S40352
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44.2	43.	42.	42.	42.	42.	41.	41.	41.	41.	40.	40.	40.	40.	40.	40.
547	532	522	521	520	519	518	513	511	507	505.5	504	504	503	499	499
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

JE0242	
Ig kappe	Ig kappa chain NIG26 precursor - human
C; Date:	C.pecies: Homo Sapiens (man) C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Access	C.Accession: JE0242
K;Allm, Submitte	K'ALIII, M.A.; Idinati, S.; Desalir, M.S.; Takeda, N.; NOJima, M.; Takasiir, 1.; Silinoda submitted to JIPID, November 1998
A; Descr	A. Description: Structure relationship of kappatype light chains with AL amyloidosis:
A; Refere	A;Reference number: JE0241 A;Accession: JE0242
A; Molecule	ule type: protein
A; Residues:	ues: 1-215 <ali></ali>
C; Superi F; 16-91,	C;bupertaminiy: immunoglobulin v region; immunoglobulin nomology F;16-91/Domain: immunoglobulin homology <imm></imm>
Query Ma Best Loc	Ouery Match 76.4%; Score 945.5; DB 2; Length 215; Best Local Similarity 83.5%; Pred. No. 1.2e-54; Masthor 183, Consorted to Michael 18, Tadels 3, Gans 1.
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qa	1 EIVLIQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPSLLIYDASSRAT 57
Qy (6	81 GVPSRFSGSGSGTDFTLTISSLOPEDFATYTCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
qQ	58 GIPDRFSGSGSGTDFILTISGLEPEDFAVYCQQYDRPPWTFGQGTKVEIKRTVAAPSVF 117
, i	111 TEDESTROLKSCTASTV/CLINNEYDREAKVOMKVINALOSGNSOFSVTEODSKISTS 200
Db 11	118 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177
Qy 2(	201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 17	
1	
RESULT JE0244	7
Ig kapp	Ig kappa chain NIG2 precursor - human
C; Specie	Cispedies: Home sapiens (man)
C; Date: C; Access	C.bate: U3-bec.1336 *sequence_revision U3-bec-1336 *text_cmange zi dan zood C.Accession: JE0244
R;Alim,	R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
A; Descri	A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A; Refere	ence number: JE0243
A; Access A; Molect	A;Accession: JE0244 A;Molecule type: protein
A;Resid	A;Residues: 1-215 <ali> C.Superfamily: immunoglobulin V region: immunoglobulin homology</ali>
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C; Accession: JE0241

E; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998

A; Pescription: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: JE0241

A; Reference number: JE0241

A; Accession: JE0241

A; Molecule type: protein

A; Residues: 1-216 < ALIX

C; Superfamily: immunoglobulin V region; immunoglobulin homology

F; 16-92/Donain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                  ;;
                                                                                                                                                              Query Match
71.6%; Score 885.5; DB 2
Best Local Similarity 81.6%; Pred. No. 9.5e-51;
Matches 177; Conservative 14; Mismatches 23.
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                   A.Molecule type: protein
A.Residues: 1-215 <LEO>
C.Superfamily: immunoglobulin V region; immuno
C.Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 79.8
Matches 174; Conservative
    preliminary
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C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Accession: JE0243
R.Alin, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998
R.Alin, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998
A. hossain and A new subgroup of k type light chains (VkV) identified in cases of AL am A. Recession: JE0243
A. Accession: JE0243
A. Accession: JE0243
A. Accession: JE0245
A. Residues: 1-215 cALI>
C. Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
F:16-90/Domain: immunoglobulin homology <IMM>
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2.1e-53;
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Best Local Similarity 81.7%; Pred. No. 6.5e-52;
Matches 179; Conservative 16; Mismatches 19
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                                                           h 74.9%; Score 926.5; Similarity 83.1%; Pred. No. 2.1e 82; Conservative 14; Mismatches
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                           Query Match
Best Local Simi
Matches 182;
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                                                                                    rat myeloma immunoglobulin kappa chain cDNP
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Wouleic Acids Res. 17, 7992, 1989
A/Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin k A/Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin k A/Accession: S06084; MUID:90016888
A/Accession: S06084
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Pred. No. 9.8e-46;
; Mismatches 52; Indels
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60.5%; Pred. No. 2.6e-42;
iive 34; Mismatches 56,
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tive 31;
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Matches 144; Conserv
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C; Species: Mus musculus (house mouse)
C; Date: 24. Aug. 1996 # Sequence_revision 13. Mar. 1997 # text_change 20-Jun-2000
C; Date: 24. Aug. 1996 # Sequence_revision 13. Mar. 1997 # text_change 20-Jun-2000
C; Accession: S68241; S68241
R; Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka. Submitted to the EMBL Data Library, March 1994
A; Description: Specific peroxidase activity by formation of an antibody L-chain-porph A; Reference number: S68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr
A;Reference number: S68211; MUID:96085223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,
FEBS Lett. 375, 273-276, 1995
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A; Description: Isolation and characterisation of sheep kappa light chain cDNA.
A; Reference number: S33161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-230 <FOL>
A; Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin F;143-212/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GVPARFSGSGSGTDFTLNIHPVEEEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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6.9e-42;
ches 47;
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N;Alternate names: immunoglobulin light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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A; Residues: 'NI', 3-212 <TAW>
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R; Foley, R.C.; Beh, K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-218 <TAK>
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A; Status: preliminary
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DB 2;

Score 748.5;

60.5%;

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A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;21-234/Product: Ig kappa chain #status predicted <MAT>F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                             Query Match
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A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr A;Reference number: JC5810; MUID: 98063277
A;Accession: JC5810
A;Molecule type: protein
A;Residues: 1-218 <AKA>
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C; Accession: 501320
R; de Waele, P: Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Blochem. 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A; Reference number: S01320; MuID:88329081
A; Accession: S01320
A; Molecule type: mRNA
A; Residues: 1-234 < DEL>
A; Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
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C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                            66 KAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQG 125
                                                                                                                                                                                               126 TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
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                    Gaps
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                                                                       DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Comment: This catalytic antibody has peroxidase oxidase. It is C:Superfamily: immunoglobulin V region; immunoglobulin homology F:16-94/Domain: immunoglobulin homology <IMM>
                      Indels
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Pred. No. 9.3e-42;
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                    Mismatches
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   Ņ.
   Pred.
                    36;
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64.78;
 62.2%;
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Matches 141; Conservative
                    145; Conservative
 Best Local Similarity
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                  Matches
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Ig kappa chain V region (17/9) - mouse

Ig kappa chain V region (17/9) - mouse

C; Species: Mus musculus (house mouse)

C; Date: 31-Mar-1990 #text_change 21-Jan-2000

C; Accession: A31790

R; Schulze-Gahmen, U; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I...

Biol. Chem. 263, 17100-17105, 1988

A; Title: Preliminary crystallographic data, primary sequence, and binding data for an A; Title: Preliminary pression: A31790

A; Reference number: A92666; MUID: 89034213

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Messidues: 1-220 <SCH>
A; Cross-references: GB: W33626; GB: J04061; NID: 9533234; PIDN: AAA39162.1; PID: 9533235

C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
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                                                                                                                                      1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMN--
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                                                     8;
     Length 234;
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C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
58.9%; Score 729; DB 2; 58.3%; Pred. No. 1.5e-40; ive 37; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.7%; Score 726; DB 2; 61.8%; Pred. No. 2.2e-40;
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                             Best Local Similarity
Matches 140; Conserv
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Search completed: August 14, 2002, 15:18:58
Job time: 686 sec
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Best Local Simi
Matches 131;
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                                          B.; Rosenbaum,
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000 C;Accession: A56169  
R;Monfardini, C.; Rieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum J. Biol. Chem. 270, 6628-6638, 1995  
A;Fitle: Recombinant antibodies in bioactive peptide design. A;Reference number: A56169; MUID:95204454  
A;Accession: A56169  
A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-210  
A;Accession: C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            If Kappa chain - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change ll-Jan-2000
C; Accession: S37484
R; Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A; Reference number: S37483
A; Rocession: S37484
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-225 < CDUC>
A; Coss references: EMBL:X70424; NID:9406254; PIDN:CAA49869.1; PID:9406255
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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61.8%; Pred. No. 9.2e-40;
iive 29; Mismatches 53;
                                                                                                                                                                                                                                                    58.0%; Score 718; DB 2;
65.1%; Pred. No. 6.8e-40;
iive 28; Mismatches 45;
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Best Local Similarity 65.1:
Matches 136; Conservative
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Matches 141; Conservative
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Forecast Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: PC4203
R; Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A; Title: Cloning and characterization of CDNAs coding for heavy and light chains of A; Reference number: PC4202; MUID:97082978
A; Accession: PC4203
A; Mulliple: Cloning A; Mulliple: Comman A; Mulliple: Comman A; Mulliple: Comman A; Mulliple: Comman Diama plasma apolipoprotein A-I of high-dense C; Comment: This protein is specific for human plasma apolipoprotein A-I of high-dense C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: C region #status predicted <CRG>
F;113-219/Domain: C region #status predicted <CRG>
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KV3J\_MOUSE
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KV3K\_MOUSE
KV1T\_HUMAN
KV1L\_HUMAN
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1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC
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Copyright (c) 1993 - 2000 Compugen Ltd.
                              OM protein - protein search, using sw model
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## ALIGNMENTS

Post-processing

Result

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		dФ			SUMMARIES			The covarence of the light chain."; acid sequence of the light chain."; Biochemistre 9:3155-3161(1970).
11t 10.	Score	Query Match Length	ength	DB	ID	Description	RR	
-	548	44.3	106	<u> </u>	TAN UITAN	001000 (m) d V01000	-	X MEDLINE=71064027; PubMed=4923144;
100	235	43.0	131		KV3I_MOUSE	of mon	RT	
ۍ 4	483	39.0	132		KV3M_MOUSE KV3M_MOUSE	P01658 mus musculu P01665 mus musculu	RL	T Intrachain disulfide bonds."; L Biochemistry 9:3188-3196(1970).
ر د	481	38.9	111		KV3N_MOUSE	9	R	
م د	480 479	38.8 38.7	111		KV30_MOUSE	P04431 homo sapien P01667 mus musculu	 R 8	
<b>&amp;</b>	478.5	38.7	129		KV3L_HUMAN	S	R.	
10	4 / 6 4 68	38.5	111		KV3Q_MOUSE KV3L_MOUSE	P01669 mus musculu P01664 mus musculu	RT	I "Rule of antibody structure. The primary structure of a monoclonal I immunoalobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
11	461	37.3	108		KV1H_HUMAN	0 homo	R	
13	458.5	37.1 36.9	110		KV3P_MOUSE	P01668 mus musculu p18136 homo sarien		
14	452	36.5	108		KV1G_HUMAN	omor 6		
16	4 4 4 4 8 4 9	36.2	108		KVIM_HUMAN	PO1605 homo sapien		
17	448	36.2	134		KV4C_HUMAN	4 homo	8	A Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
9 5	446	36.1	108		KV1B_HUMAN		RT	"Cloned human and mouse kappa immunoglobulin constant
20	445	36.0	108		KV1F_HUMAN	PO1597 nomo sapien PO1598 homo sapien		
21	445	36.0	108		KV1N_HUMAN	bomo	RN	
23	447	35.7	108		KVIV_HUMAN	PO4430 homo sapien DO1593 homo sapien	RP	P SEQUENCE (BENCE-JONES PROTEIN ROY).
24	441	35.7	117		KV1J_HUMAN	2 homo	RA	
25	436	35.2	111		KV3H_MOUSE	_	RL	L (In) Franek F., Shugar D. (eds.);
97	435	35.2	108		KV10_HUMAN	7 homo	RL	
28	432.5	35.0	133		KVIF_HUMAN	POI6U8 homo sapien	RE	L New York (1969). N FAI
29	431.5	34.9	129		KV3H HIMAN	7 homo	90	- 0,
30	430	34.8	108	ı ٦ ·	KV1Y_HUMAN	2 homo	RX	
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33	429 429	34.7	129		KV1S_HUMAN KV1X_HUMAN	P01611 homo sapien P04432 homo sapien	RT	<pre>T "The complete amino acid sequence of Bence Jones protein Cum (kappa- I type).";</pre>

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SEQUENCE OF 1-35.
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                   Titani K., Shinoda T., PubMed-4893682;

"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";

[8] Biol. Chem. 244:3550-3560(1969).
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                                                                                                                                                                Science 169:56-59(1970).
-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER, 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                               Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH A HEAVY CHAIN).
V -> L (IN INV(1,2) MARKER).
/FIId-VAR_003897.
D -> N (IN REF. 7 AND 8).
E -> Q (IN REF. 5 AND 6).
51984D1FDD372CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.3%; Score 548; DB 1; Length 106; 100.0%; Pred. No. 1.8e-37; ive 0; Mismatches 0; Indels
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
If kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse).
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                                                                                                        SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU). MEDLINE-70201507; PubMed-5447531;
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57 E
11609 MW;
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InterPro; IPR003597; Ig_cl.
Pfam; PF00047; Ig. 1.
SMART: SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
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Matches 106; Conservative
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KV31_MOUSE
ID KV31_M
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DT 21-JUL,
DT 21-JUL,
DE 15 AUT,
DE 15 AUT,
DE 16 AUT,
OC BURATY,
OC MARMAN
OX NCBL_T.
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MEDLINE-79012520; PubMed-99744;
MCDLINE-79012520; PubMed-99744;
McChanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PTS: A01935; KVMSM6.
HSSP, PO1789; LMCP.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Ffam. PF00047; ig. 1.
SMART; SM00406; IGV; 1.
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Was musculus (Mouse).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                      McKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Blochemistry 12:760-771(1973).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAPPA CHAIN V-III REGION MOPC 63.
MEDLINE-78235887; PubMed-98179; Burstein Y., Schechter I.; Burstein Y., Schechter I.; The Parliary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%; Score 532; DB 1; 75.6%; Pred. No. 4.6e-36; tive 18; Mismatches 14;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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BY SIMILARITY.
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MEDLINE=73140225; PubMed=4691517;
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Best Local Similarity
...hes 99; Conserva
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|121 TFGGGTKLEIK 131
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131
131 AA;
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21 DIVLIQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
Loh E., Schilling J., Hood L.E.; information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                         81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                            Length 111;
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                                                                                                                                                                                                                                          12002 MW; 7A5FCB586C306D29 CRC64;
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                                                                                                                                                                                                                                                                            39.0%; Score 483; DB 1; ilarity 81.1%; Pred. No. 3.1e-32; Conservative 10; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region PC 7183.
Mus musculus (Mouse).
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                                                                                                                                                                                                                  BY SIMILARITY.
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BY SIMILARITY
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HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003596; Ig_V.
Ffan; PF00047; Ig'. ISMART; SMO0406; IGV; 1.
Immunoglobulin V region.
                                             PIR; A01937; KVMS43.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Weigert M., Gatmaitan L., "Rearrangement of genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11952
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Nature 276:785-790(1978).
                                  Nature 276:785-790(1978).
                                                                                                                    Immunoglobulin V region
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Matches 90; Conserv
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P01666;
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KV3N_MOUSE
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                                                                                                                                                                             Biochemistry 12:749-759(1973).
-!- MISCELLANEDUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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                                                                                                                   SEQUENCE OF 21-132.
MEDLINE-7314024; PubMed-4120629;
MEDLINE-7314 Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 METDTILLEWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                                                                                          IG KAPPA CHAIN V-III REGION MOPC 321.
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Was musculus (Mouse).
Washaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                Burstein Y., Schechter I.; "Primary structures of N-terminal extra peptide segments linked "Primary structures of N-terminal extra pertable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7043.
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                                                                                 expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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MEDLINE=79073152; PubMed=103003;
          SEQUENCE OF 1-37.
MEDLINE=78235887; PubMed=98179;
                                                                                                                                                                                                                                       PIR; A01933; KVMS32.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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132 AA;
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P01665;
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P18135;
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KV30_MOUSE
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                      Gaps
                                                       Gaps
                                          21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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                                                                                                                                                                                                                                                                                                     Klobeck H.G., Combriato G., Zachau H.G.;
Immunoglobulin genes of the Kappa light chain type from two human
Imphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Walker precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-I REGION WALKER. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                 81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRFFGQGTKVEIK 131
  Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK - 3.
COMPLEMENTARITY - DETERMINING - 3.
FRAMEWORK - 4.
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                      11; Indels
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38.9%; Score 481; DB 1;
80.2%; Pred. No. 4.5e-32;
ive 11; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.8%; Score 480; DB 1; 74.0%; Pred. No. 6.5e-32; iive 12; Mismatches 18;
                                                                                                                                                               129 AA
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                                                                                                                                                                                                                                                                                            MEDLINE=85014148; PubMed=6091049;
                     89; Conservative
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          Similarity
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129 AA;
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59 QOKPGKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLI 118
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                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 111;
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80.2%; Pred. No. 6.4e-32;
iive 10; Mismatches 12
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region HAH precursor.
                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 6308.
                                                                                                                                                                                                                                                 111 AA.
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BY SIMILARIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 276:785-790(1978).
PIR; C01937; KWMS08.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffan; PF00047; Ig; I.
SWART; SM00406; IGv; I.
Immunoglobulin V region.
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Best Local Similarity 80.28
Matches 89; Conservative
                                                                                                                                                                                                                                                    STANDARD;
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119 TFGQGTRLEIK 129
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P01664;
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Best Local S
Matches 88
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
*Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MATOMONITBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-III REGION HAH.
FRAMEWORK-1.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14073 MW; D3C55292772774D0 CRC64;
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68.9%; Pred. No. 8.5e-32;
ive 17; Mismatches 21
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7769.
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BY SIMILARITY
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity 68.99
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AA;
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P01669;
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**XEMILINE=79012520; PubMed=99744;

**MCKean D.J., Bell M., Potter M.;

**Telated mouse kappa variable regions.";

**Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

**RISSP: PO1789; IMCP.

**INTERPRO: IPR003306; Ig_MC.

**RISSP: PO1789; Ig_V.

**RISSP: PO1789; Ig_V.

**RISSP: PO1789; Ig_V.

**RISSP: MCO.** IG_V.

**MILL MCO.** IG_V.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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COMPLEMENTARITY - DETERMINING - 1.
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   FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.5%; Score 476; DB 1; Length 111; 79.3%; Pred. No. 1.1e-31;
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                            COMPLEMENTARITY-DETERMINING-2.
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; Pred. No. 4.9e-31;
12; Mismatches 12;
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15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CBPC 101.
Mus musculus (Mouse).
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21-JUL-1986 (Rel. 01, Last seq
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78.4%;
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
                                      PIR; D01937; KVM510.
HSSP, P01789; IMCP.
InterPro; IPR003906; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                          11950 MW;
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Best Local Similarity 78.48
Matches 87; Conservative
                    diversity.";
Nature 276:785-790(1978).
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110 AA;
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  Weigert M.,
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KV3M_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                  MEDLINE-71032830; PubMed-4097974; Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 461; DB 1; Length 108;
; Pred. No. 1.7e-30;
11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING - 2.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7210.
                                                                                                                                                                                                                                                                                                                                Immunoglobulin V region; Bence-Jones protein.
DOMAIN 1 23 FRAMEWORK-1.
                                                            108 AA
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35 49 50 56 7 88
7 97 97 107 108 108 108
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                                                                                                             Ig kappa chain V-I region Hau.
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80.4%;
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                                                            STANDARD;
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                                                                                                                                                      NCBI_TaxID=9606;
                                                            KV1H_HUMAN
P01600;
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P01668;
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KV1H_HUMAN
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167.840-852(1988).
-: DISERABE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARIITY-DETERMINING-1.
                    COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY - DETERMINING - 2.
FRAMEWORK - 3.
                                                                           COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                 69F1A5CE886B1249 CRC64;
                                                                                                                                                                                                                                                                                                                               37.1%; Score 458.5; DB 1;
78.4%; Pred. No. 2.8e-30;
tive 11; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Homo sapiens (Human).
FRAMEWORK-1.
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                                                       FRAMEWORK-2
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HSSP, POLT98; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Fram; PP0047; 19; 1.
SMART; SM00406; IGv. 1.
Immunoglobulin V region; Signal.
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81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132

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Laure C.J., Watanabe S., Hilschmann N.;
Taure C.J., Watanabe S., Hilschmann N.;
The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I., The amino acid sequence of the L-chain of
kappa-type, subgroup I., The amino acid sequence of the L-chain of
HODPOS-SEYIEV'S Z. Physiol. Chem. 354:1503-1504(1973).
-!- MISCELLANEOUS: THE CREGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                    Gaps
                                                                                                    1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                                       3;
                                                                DB 1; Length 129;
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
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Pred. No. 9e-30;
8; Mismatches 11; Indels
                                                              ch 36.9%; Score 456.5; DB 1; Length I Similarity 67.4%; Pred. No. 4.9e-30; 89; Conservative 17; Mismatches 23; Indels
                                     14070 MW; 7395528EA2BB74D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; Clad3CB0F600FF73 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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79.5%;
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HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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*** MEDLINE-77038198; PubMed=824717;

*** REDLINE-77038198; PubMed=824717;

*** REDLINE-77038198; PubMed=824717;

*** Capra J.D., Klapper D.G.;

*** Capra J.D., Klapper D.G.;

*** Capra Mind and a globulins (Lay/Pom) with shared idiotypic

*** Tym and 1-gamma globulins (Lay/Pom) with shared idiotypic

*** Tym and 1-gamma globulins (Lay/Pom) with shared idiotypic

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-3.
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78.6%; Pred. No. 1.6e-29;
.ive 8; Mismatches 12; Indels
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34 COMPLEMENTARITY-DETERMINING-49 FRAMEWORK-2.
56 COMPLEMENTARITY-DETERMINING-88 FRAMEWORK-3.
97 COMPLEMENTARITY-DETERMINING-107 FRAMEWORK-4.
88 BY SIMILARITY.
108 BY SIMILARITY.
108 BY SIMILARITY.
KVIM_HUMAN STANDARD; PRI; 108 AA. P01665; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-I region Lay.
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sp\_vertebrate:\*
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sp\_virus:\*

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sp\_archeap:\*

sp\_mhc:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\* sp\_rodent:\*

SUMMARIES

Result ٠ و

Q99m37 mus musculu Q91wf8 mus musculu Q91ws9 mus musculu Q9rla5 mus musculu Q91w12 mus musculu Q91w17 homo sapien Q9u177 homo sapien Q9u179 homo sapien Q9u179 homo sapien Q90pf6 homo sapien Q90pf6 mus musculu Q96ee1 homo sapien Q920e9 mus musculu Q920e9 mus musculu Q910e0 mus sapien Q920e9 mus sapien Q920e9 mus sapien Q92u178 homo sapien Description Q91WF8 Q91WS9 Q91R1A5 Q91W12 Q91XL0 Q9UL77 Q96SA9 Q9UL70 Q99M11 099M37 Q9UL79 Q96PF6 Query Match Length DB 660.3 559.7 559.7 557.0 557.0 557.0 337.5 337.5 34.5 34.9 746.5 Score

11110987654321 111110987654321

**Q96E61** 

34.7 33.5 31.9

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Gaps

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60.3%; Score 746.5; DB 11; Length 238; 58.5%; Pred. No. 1.5e-57; ive 40; Mismatches 56; Indels 1;

Query Match
Best Local Similarity 58.59
Matches 137; Conservative

Q96169 homo sapien Q9u183 homo sapien Q9u183 homo sapien Q9u186 homo sapien Q9u186 homo sapien Q9u186 homo sapien Q9u186 mus musculu Q92569 mus musculu Q9u180 homo sapien Q9u10 schistosoma Q9u10 schistosoma Q9u10 mus musculu Q9178 mus musculu Q9178 mus musculu Q9182 mus musculu Q9184 mus musculu Q9182 homo sapien Q9184 mus musculu Q9184 mus musculu Q91851 homo sapien Q96561 homo sapien Q96511 homo sapien Q96512 homo sapien Q96512 homo sapien Q96512 homo sapien Q96512 homo sapien Q96512 homo sapien Q96512 homo sapien	pdate) update) update)  tebrata; Euteleostomi;  Muridae; Murinae; Mus.  7 MONTHS OLD, GROSS  BJ databases.
096169 090KB0 090XF0 0910485 0910485 0910486 0910486 0910480 0910480 0910410 0910484 0931A6 0931A6 0931A6 0931A6 0931A84 0931A84 0931A84 0931A84 0931B84 0931B84 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0 090KB0	A. upda n upda i
30.9 233 4 30.7 108 4 30.6 238 111 30.0 29.8 1 30.0 109 4 30.0 109 4 30.0 109 4 22.5 109 111 28.4 1127 11 28.0 107 11 26.5 5 97 111 26.6 5 97 111 26.7 109 6 24.7 109 6 24.7 109 6 24.7 109 6 24.7 109 6 19.3 107 4 18.2 107 11 19.6 107 11 19.6 107 11 19.6 107 11 19.6 107 11 19.7 11 267 13	NARY; rel. 17 rel. 17 rel. 17 rel. 17 Chorda Chorda R. WAP- R. WAP- 19 to th 02035.1 19 to th 19 to th 19 to th 11 to th
17 382.5 18 380 20 377 21 371.5 22 371.5 24 366 27 366 28 351 28 351 29 351 30 345 31 328.5 31 328.5 32 328 34 306 34 5 37 243 38 238.5 39 236.5 40 235.5 41 225 42 207.5	RESULT 1  Q99M37  AC Q99M37  DT 01-JUN-2001 (TFEMBL DT 01-JUN-2001 (TFEMBL DT 01-DEC-2001 (TFEMBL DE HYPOTHETICAL 26.3 K  MUS musculus (Mouse OC Bukaryota; Metazoa; OC Bukaryota; Metazoa; OC Mammalia; Eutheria.  (1) Eustryota; Metazoa; OC Mammalia; Eutheria.  KP SEQUENCE FROM N.A.  RP SEQUENCE FROM N.A.  RC TISSUE.  RA STRAUSBERG K.; DR HASPE, PO1679; ZBBJ. DR INTERPIC; IPR003599 DR INTERPIC; IPR003599 DR SMART; SM00400; IGS DR SMART; SM00400; IGS DR SMART; SM00410; IGG DR SWART; SM0041

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Strausberg R.;
Submitted (SEP-2001) to the
EMBL; BC013496; AAH13496.1;
                                                                                                      Hypothetical protein.
NON_TER 1
SEQUENCE 233 AA; 2
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  SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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                                                                                                                                                                                                121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                                                                            65 GOSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEABDLGVYYCFQGSHVPYTFGS 124
                                                                                                                                                                       125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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  64
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
6 ILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDY-DGDSYMNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausherg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015592; AAH15292.1; -.
Hypothetical protein.
SROUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 25.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%; Score 739; DB 11;
60.1%; Pred. No. 6.6e-57;
iive 33; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Q91WS9;
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"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scrV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF152371; AA040242.1;
HSSP; P01679; ZFBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 LIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                          131 KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                  11 LLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKL 70
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                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                        59.7%; Score 738; DB 11; Length 233; 63.2%; Pred. No. 8e-57; 1.ve 28; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 233
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EMBL/GenBank/DDBJ databases
                                                                                                            233 AA; 25781 MW; BIC184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52BA205FDE995E2A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 58.6%; Score 725; DB 11; Best Local Similarity 63.3%; Pred. No. 9.8e-56; Matches 138; Conservative 30; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPLO: TPR003600; Ig_like.
INTERPLO: IPR003006; Ig_MHC.
INTERPLO: IPR003596; Ig_v.
Pfam: PF00047; Ig; 2.
SMART; SM00406; IGv.
PR0SITE; PS002400; IG_like; I.
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                                                                                                                                                                                                                        Best Local Similarity 63.29
Matches 144; Conservative
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SEQUENCE FROM N.A.
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                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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LESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                               STGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUB-KIDNEY;
Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae; Mus
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                    57.0%; Score 705.5; DB 11; Length 235; 61.1%; Pred. No. 5.7e-54; ive 31; Mismatches 50; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TIEMBLIEL. 19, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
ADULT MALE KIDNEY CDNA, RIKER FULL-LENGTH ENRICHED LIBRARY,
CLONE: 0610010P20, FULL INSERT SEQUENCE.
Mus musculus (Mouse).
Eukaaiyota Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Nammalla; Butheria; Rodentia; Sciurognathi; Muridae; Mutina
                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006643; AAH06643.1; -. SEOUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                            091W12 PRELIMINARY; PRT; 235 cm.
091W12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:6582).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091XLO;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 61.19
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
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Q91W12
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Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE=20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDILINE-21085660; PubMed-11217851;
RIKEN FRATOM CONSORtium.;
"Functional annotation of a full-length mouse cDNA collection.";
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EMBL; AK002514; BAB22154.1;
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Pred. No. 6.7e-54;
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MEDLINE-99279253; Pubmed-10349636;
Carnincl P., Hayashizaki Y.;
Carnincl P., Hayashizaki Y.;
Mith-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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61.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMIQSPSSLSASVGDRVIITCRASQSI----SSYLNWYQQKPGKAPNLLIYAASSLQS
                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934; Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
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SEQUENCE FROM N.A.
MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL: U96396; AAB68785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 463.5; DB 4; Length 107;
Pred. No. 3e-33;
6; Mismatches 7; Indels 5,
                                                                                                                                                                                                                                                                                                                                                     Score 471; DB 4; Length 108; Pred. No. 6.8e-34;
                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                               8; Indels
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108 AA: 11738 MW; C06681716C4D16F3 CRC64;
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EMBL; AF035037; AAD56273.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 19; 1.
Pfam; CM00407; 19; 1.
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83.0%;
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Best Local Similarity 83.9%;
Matches 94; Conservative
                       01-MAY-2000 (TrEMBLrel. 13,
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 PRELIMINARY;
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                                                                                 Homo sapiens (Human)
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107 AA;
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Best Local Similarity
                                                                                                                   NCBI_TaxID=9606;
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Q96SA9;
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                         21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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                                                                                                                          81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
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MEDILINE-99277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.4%; Score 450; DB 4; Length 108; larity 78.6%; Pred. No. 4.7e-32; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                 81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelk
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
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InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
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108 AA;
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Best Local Similarity
Matches 88; Conserv
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                              Score 438.5; DB 4; Length 107;
Pred. No. 4.7e-31;
9; Mismatches 10; Indels 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                             81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.3%; Score 437; DB 4; Length 108; 77.7%; Pred. No. 6.4e-31; ive 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                            107
107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF03503; AAD56269.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
NON_TER.
IND_TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87; Conservative
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                        SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                 Local Similarity
les 88; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                           ; ig;
                                                                                                                                     Pfam; PF00047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                Query Match
Best Local S
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
Q9UL79
                                                                                                                                                                                                                                                                                                                      Matches
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81 GVPSRFSGSGSGTDFTLFISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                           MEDLINE-21361171; PubMed-11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; contributions of organ involvement in primary systemic amyloidosis: contributions of IG V(L) germ line gene use and clonal plasma cell burden."; Blood 98:714-720(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.0%; Score 433; DB 4; Length 116; 70.8%; Pred. No. 1.6e-30; Live 14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JAN 2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 116
116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
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                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.4 KRA PROFEIN.
Mus musculus (Mouse).
  116 AA.
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SMART; SM00409; IG; 2.
SMART; SM004067; IGC1; 1.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_11ke; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF361758; AAK51465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 235 AA; 2
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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Best Local Si
Matches 85;
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                                                                                                                                                                                                                                     67 APKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ--QSNEDPRTFGQ 124
                                                                                                                                                                                                    67 APKLLIYAASNLESGVPSRFSGS--GSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                  125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGN 182
                                                                                                                    Gaps
                                Gaps
                                                                                      7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLTLLAHCTGSWAQSVLAQ-PPSVSGAPGOTVTISCTGS-STNIGAGYAVHWYQQFPGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                 184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 APKVLIYGNYNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNKNOWN (PROTEIN FOR MGC:17259).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-MIMICKING ANTI IDIOTOPE KAPPA CHAIN VARIABLE REGION
                                Indels
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Straubberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;
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SEQUENCE FROM N.A.
TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       096E61;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
5.4e-30;
ches 86;
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42.6%; Pred. No. 5.4e
:ive 37; Mismatches
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Best Local Similarity 42.69
Matches 101; Conservative
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Q96E61
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Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                              21 DIVLIQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                               Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                               Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF307935; AAL09419.1; -. NON_TER
                                                                                                                                                                                                                               111
12046 MW; 1E46988AA6858526 CRC64;
                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                               Query Match 33.5%; Score 415; DB 11; Best Local Similarity 72.1%; Pred. No. 5.6e-29; Matches 80; Conservative 12; Mismatches 19;
                                                                                                                                                                                                                               111 1
111 AA;
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NON_TER
SEQUENCE
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Description	Humanised anti-Fas	Humanisca anti-fas Humanisca anti-fas	Humanised anti-Fas	Humanised HFE7A de Anti-Fas humanised	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas
SUMMARIES	AAW90931 AAW90930	AAW90932	AAB14777	AAW83031	AAB14772 AAW90922	AAW83032	AAB14773
DB	21	21	21	21 19	21	13	21
% Query Match Length DB	238	238	238	238 238	238	238	238
& Query Match	100.0	99.6	95.1	95.1	94.7	93.7	93.7
Score	1237	1232	1177	1177	1172	1159	1159
Result No.	17	ı m 🔻	יטי	9	ထတ	10	11

99EP-0307711. 98JP-0276881. 98JP-0276882.

29-SEP-1999; 30-SEP-1998; 30-SEP-1998;

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(SANY ) SANKYO CO LTD.

humanised HFPA d Anti-Fas humanised Anti-Fas humanised Humanised anti-Fa Human E27 anti-Ig Mus musculus anti Human IGFAM-10 im Human IGFAM-10 im Human IGFAM-10 im Human IGFAM-10 im Human immune reap Sequence of the k Human IGFAM-10 im Human anti-Fa Sequence Musculus antiatreriosoclerotic; ystemic lupus erythematosus; is; graft versus host disease; is graft versus host disease; is graft versus host disease; is sterility; myasthenia gravis; is tromobopenia purpura; allergy; epatitis; transplant rejection.	13	1159 1158 1158	93.7 93.6 93.6	238 238 238	21 19 21	AAW90923 AAW83035 AAB14778	Humanised anti-Fas Anti-Fas humanised Humanised anti-Fas
1157   93.5   238   19   AAN#9303     1157   93.5   238   19   AAN#9303     1157   93.5   238   21   AAN#9363     1106   89.6   218   21   AAN#9563     1006   88.6   218   21   AAN#9563     1007   86.6   218   22   AAN#9560     1073   86.7   218   20   AAN#9560     1073   86.7   218   22   AAN#9560     1070   86.5   218   22   AAN#9560     1070   86.5   218   22   AAN#9561     1070   86.5   218   22   AAN#9651     1071   86.5   218   22   AAN#9651     1070   86.5   218   22   AAN#9651     1071   86.5   218   22   AAN#9651     1070   86.5   218   22   AAN#9651     1071   86.5   218   22   AAN#9651     1070   86.5   218   22   AAN#9651     1071   86.5   218   22   AAN#9651     1071   86.5   218   22   AAN#9651     1072   86.5   218   22   AAN#9651     1071   82.7   240   20   AAX#961     1072   82.7   240   22   AAN#9651     1073   83.8   23.7   24   AAN#9630     1071   82.7   24   236   16   AAN#9651     1071   82.7   24   236   16   AAN#9651     1071   82.5   237   21   AAN#9630     1071   82.5   237   21   AAN#9630     1071   82.5   237   21   AAN#9630     1071   82.5   237   24   AAN#9650     1072   82.5   237   24   AAN#9650     1073   82.5   237   24   AAN#9650     1074   82.5   237	14	1158	93.6	238	21	AAB14778 AAW90928	anti-E HFE7A
1157 93.5 238 21 AABHJ74   1157 93.5 238 21 AABHJ74   1168 89.6 218 18 AAW13563   1096 88.6 218 18 2 AAW505024   1108 89.6 218 18 2 AAW50502   1096 88.6 218 22 AAB76504   1073 86.7 218 20 AAW50560   1070 86.5 218 20 AAW50560   1070 86.5 218 20 AAW50560   1070 86.5 218 22 AAB7087   1070 86.5 218 22 AAB7087   1070 86.5 218 22 AAB70593   1070 86.5 218 22 AAB70528   1070 86.5 218 22 AAB70593   1070 86.5 218 22 AAB70503   1070 86.5 218 22 AAB70503   1070 86.5 218 22 AAB70503   1070 86.5 218 22 AAB70508   1070 86.5 218 22 AAB70503	16	1157		238	19	AAW83033	umanis
1106   89.6   218   18   AAW13563     1096   88.6   218   21   AAW35658     1096   88.6   218   22   AAW35658     1096   88.6   218   22   AAW35658     1096   88.6   218   22   AAW35650     1073   86.7   218   20   AAW35660     1070   86.5   218   22   AAB76919     1070   86.5   218   22   AAB76951     1070   86.5   218   22   AAB76950     1040   86.5   218   22   AAB76950     1041   84.7   240   20   AAX36160     1041   84.7   240   20   AAX36160     1041   84.7   240   20   AAX36160     1041   84.7   241   24   241   24     1045   84.8   237   21   AAB83912     1041   82.7   240   22   AAB76930     1042   82.7   240   22   AAB76930     1031   82.7   240   22   AAB76930     1032   82.7   240   22   AAB76930     1031   82.7   240   22   AAB77614    AUG-2000 (first entry)   antibody; human; anti-inflammatory; anti-anemic; anti-anemic; anti-anemic; anti-arthritic; homanized; anti-arthritics; homanized; homanized; anti-arthritics; homanized; homanized; homanized; anti-arthritics; homanized; homani	17	1157		238	21	AAB14774	anti
1096 88.6 218 20 AAM95058 1096 88.6 218 20 AAM95058 1096 88.6 218 22 AAB5200 1073 86.7 218 20 AAW95660 1070 86.5 218 20 AAW95669 1070 86.5 218 20 AAW95669 1070 86.5 218 22 AAB76948 1070 86.5 218 22 AAB76958 1070 86.5 218 22 AAB76958 1049.5 84.8 237 21 AAY96289 1040.5 84.8 237 21 AAY96289 1041.5 84.2 234 18 AAW11638 1021 82.5 237 21 AAY96289 1041.5 84.2 234 18 AAW11638 1023 82.7 24 AAW3873 1019 82.4 236 16 AAR77614  AALGAMENTS  AUG-2000 (first entry) anised anti-ras designed light chain Leu 2 protein. ; antibody; human; anti-inflammatory; artiviral; amtiar autological; immunosuppressive; thyromimetic; antiar autological; immunosuppressive; thyromimetic; antiar autological; immunosuppressive; thyromimetic; antiar autoropic; humanized; apoptosis; systemic lupus ery himoto disease; rheumatoid arthritis; graft versus fright sclerosis; Basedow's disease; thrombopenia pull m dependent diababetes mellitus; arteriosclerosis; ulind mellinopethritis; hepatitis; transplithentic.	13	1108		218	18	AAW13563	anti
1000 88.6 218 21 AAB76947 1009 88.0 218 12 AAB76947 1009 88.0 218 14 AAR33312 10073 86.7 218 20 AAW95660 10073 86.7 218 20 AAW95660 10073 86.7 218 20 AAW95660 10073 86.7 218 20 AAW95669 10070 86.5 218 22 AAB7421 10070 86.5 218 22 AAB76949 10070 86.5 218 22 AAB76951 10070 86.5 218 22 AAB76951 10070 86.5 218 22 AAB76953 10070 86.5 218 22 AAB76951 10070 86.5 218 22 AAB77614 AAR39162 10070 86.5 218 20 AAW7791 AAR39162 10070 86.5 20.0 AAW7791 AAR3917 AAR3	200	1096		218	200	AAWYS658	Mus musculus anti- Ticht chain amino
1089 88 0 218 14 AAR3312 1073 86.7 218 20 AAW95660 1073 86.7 218 20 AAW95660 1073 86.7 218 20 AAW95660 1073 86.7 218 21 AAB97472 1070 86.5 218 22 AAB74211 1070 86.5 218 22 AAB77087 1070 86.5 218 22 AAB77087 1070 86.5 218 22 AAB76949 1070 86.5 218 22 AAB769591 1070 86.5 218 22 AAB769691 1070 86.5 218 22 AAB769491 1070 86.5 218 22 AAB769491 1070 61.5 41.2 41.2 41.2 AAB879162 1070 61.5 41.2 41.2 41.2 AAB879162 1070 61.5 41.2 41.2 AAB879162 1070 61.5 41.2 41.2 41.2 AAB77614 1070 86.5 218 22 AAB77614 1070 61.5 41.2 41.2 41.2 41.2 41.2 41.2 41.2 41.2	22	1096		218	22	AAB76947	Full variable ligh
10/3 86.7 218 20 AAM95660 1073 86.7 218 20 AAM95660 1073 86.7 218 20 AAM95660 1070 86.5 218 20 AAM95669 1070 86.5 218 20 AAM95669 1070 86.5 218 20 AAM95669 1070 86.5 218 22 AAB76949 1070 86.5 218 22 AAB76949 1070 86.5 218 22 AAB76951 1070 86.5 218 22 AAB76959 1049.5 84.8 237 21 AAB76593 1049.5 84.8 237 21 AAM9669 1041.5 84.4 24.1 22 AAM9669 1041.5 84.4 24.1 22 AAM9689 1041.5 84.4 24.1 22 AAM9689 1041.5 84.4 24.1 22 AAM9689 1041.5 84.5 237 21 AAM9689 1041.5 84.5 237 21 AAM9689 1051 83.8 237 21 AAM9689 1051 83.8 237 21 AAM9689 1051 82.5 237 21 AAM9689 1051 82.5 237 21 AAM9689 1051 82.5 237 21 AAM9689 1051 82.6 237 21 AAM9689 1051 82.9 237 21 AAM9689 1052 83.9 237 21 AAM9689 1052 83.9 237 21 AAM9689 1053 83.9 237 21 AAM9689 1051 82.4 236 16 AAM77614 1019 82.4 236 16 AAM77614 1019 82.4 236 16 AAM7873 1019 82.4 24 24 24 24 AAM7873 1019 82.4 24 24 24 24 AAM7873 1019 82.4 24 24 24 24 24 24 24 24 24 24 24 24 24	23	1089		218	14	AAR33312	Humanised MaE11 Ve
1073 86.7 218 20 AAW95662     1073 86.7 218 21 AAB07472     1070 86.5 218 22 AAB74211     1070 86.5 218 22 AAB76949     1070 86.5 218 22 AAB76949     1070 86.5 218 22 AAB769591     1071 84.5 237 21 AAY96289     1045.5 84.6 237 21 AAY96301     1045.5 84.4 24 24 12 AAB7614     1045.5 84.5 237 21 AAY96301     1037.5 83.9 237 21 AAY96301     1037.5 83.9 237 21 AAY96301     1037.5 83.9 237 21 AAY96301     1031 82.5 237 20 AAW73873     1021 82.5 237 20 AAW73873     1022 82.7 240 2240     234 18 AAW73873     1031 82.4 236 16 AAR77614     2406-2000 (first entry)     anised anti-ras designed light chain Leu 2 protein.     30931; Autinfertility neuroprotective; antiaratological, attinfertility; adisase; sterility; myas tiple sclerosis; Basedow's disasas; thrombopenia pulin dependent diabetes mellitus; arteriosclerosis; lipid sclerosis; and and adisabetes mellitus; arteriosclerosis; thatic.	4 6	1073		218	200	AAM95660	Mus musculus anti-
1073 86.7 218 21 AAB07472 1073 86.7 218 22 AAB7211 1070 86.5 218 22 AAB7664 1070 86.5 218 22 AAB7664 1070 86.5 218 22 AAB7664 1070 86.5 218 22 AAB76659 1070 86.5 218 22 AAB76951 1070 86.5 218 22 AAB76959 1040.5 84.8 237 21 AAY86289 1041.5 84.4 24 12 AAB82012 1041.5 84.4 24 12 AAB82012 1041.5 84.4 24 12 AAB82012 1041.5 84.9 237 21 AAY86301 1037 82.9 237 21 AAY86301 1038 83.8 234 18 AAW11638 1019 82.4 236 16 AAB77614 1019 82.4 236 237 20 AAW73873 1019 82.4 236 237 20 AAW73873 1019 82.4 236 16 AAB77614 1010 62.5 237 20 AAW73873 1019 82.4 236 16 AAB77614 1010 62.5 237 20 AAW73873 1019 82.4 236 16 AAB77614 1010 62.5 237 20 AAW73873 1019 82.4 236 16 AAB77614 1010 62.5 237 20 AAW73873 1019 82.4 236 16 AAB77614 1010 62.5 237 20 AAW73873 1019 82.4 236 16 AAB77614 1010 62.5 237 20 AAW73873 1019 82.4 236 25 24 24 25 2	26	1073		218	20	AAW95662	Mus musculus anti-
1073 86.7 218 22 AAB74211 1070 86.5 218 20 AAB95669 1070 86.5 218 22 AAB47087 1070 86.5 218 22 AAB47087 1070 86.5 218 22 AAB76919 1070 86.5 218 22 AAB76951 1049.5 84.8 237 21 AAY96289 1043.5 84.5 237 21 AAY96289 1043.5 84.5 237 21 AAY96301 1037.5 83.9 237 21 AAY96301 1037.5 83.9 237 21 AAY96301 1023 82.7 240 22 AAB77614 1019 82.4 236 16 AAB77614 1021 82.5 237 20 AAW73873 1019 82.4 236 16 AAR77614 1019 82.5 237 22 AAB7600000000000000000000000000000000000	27	1073		218	21	AAB07472	Amino acid sequenc
1070 86.5 218 20 AAM95664 1070 86.5 218 22 AAB76951 1070 86.5 218 22 AAB76951 1070 86.5 218 22 AAB76951 1070 86.5 218 22 AAB76953 1070 86.5 218 22 AAB76953 1070 86.5 218 22 AAB76953 1070 86.5 218 22 AAB76959 1070 86.5 218 22 AAB76959 1040.5 84.8 237 21 AAY96289 1041.5 84.7 240 22 AAB76289 1041.5 84.2 234 14 AAR39162 1041.5 84.2 234 14 AAR39162 1037 83.9 237 21 AAY96289 1037 83.9 237 21 AAY9639 1039 82.4 240 22 AAG63665 1021 82.5 237 20 AAW7873 1019 82.4 236 16 AAR77614  ALIGNMENTS  1023 82.7 240 22 AAG63665 1021 82.5 237 20 AAW7873 1019 82.4 236 16 AAR77614  ALIGNMENTS  1040.5 AAR3900000000000000000000000000000000000	78	1073		218	2 5	AAB74211	E27 anti-IgE antib Mus musculus anti-
1070 86.5 218 22 AAB47087     1070 86.5 218 22 AAB47087     1070 86.5 218 22 AAB76951     1070 86.5 218 22 AAB76953     1040.5 84.5 218 22 AAB76958     1041.5 84.2 237 21 AAY96209     1041.5 84.2 234 14 AAR38162     1037.5 83.9 237 21 AAY96301     1036 83.9 234 18 AAM1638     1037 83.9 237 21 AAX96301     1038 82.7 240 22 AAG8365     1039 82.4 236 16 AAM73873     1019 82.5 237 22 AAM73873     1021 82.5 237 22 AAM73873     1022 82.5 237 22 AAM73873     1036 82.4 236 16 AAR77614     1046-2000 (first entry)     antibody; human; anti-inflammatory; anti-anemic; antibody; human; anti-inflammatory; anti-arthritic; antiviral; immunomodula matological; lumunosuppressive; thyromimatic authorogenic; antinfertility; neuroprotective; antiamatorogical; numanized; apoptosis; systemic lupus ery himoto disease; thrombopenia put himoto disease; thrombopenia put lipule sclerosis; abasedow's disease; thrombopenia put lipule sclerosis; abasedow's disease; thrombopenia put lipule sclerosis; basedow's disease; thrombopenia put lipule disbetes mellitus; arteriosclerosis; thetic.	0 6	1070		218	9 0	AAW95664	Mus musculus anti-
1070 86.5 218 22 AAB76949 1070 86.5 218 22 AAB76951 1070 86.5 218 22 AAB76953 1070 86.5 218 22 AAB76953 1040.5 84.8 237 21 AAY96299 1041.5 84.4 237 21 AAY96289 1041.5 84.4 237 21 AAY96301 1041.5 84.2 234 14 AAR38162 1036 83.9 237 21 AAY96301 1036 83.8 234 24 AAR38162 1037 5 83.9 237 21 AAY96301 1031 82.5 237 22 AAW71838 1031 82.7 240 22 AAG63665 1021 82.5 237 24 AAW71837 1019 82.4 236 16 AAW77614 1019 82.4 236 16 AAR77614 1010 82.4 236 16 AAR77614 1021 82.8 AAR77614 1021 82	31	1070		218	22	AAB47087	Anti-IgE antibody,
1070 86.5 218 22 AAB/76951 1070 86.5 218 22 AAB/76958 1070 86.5 218 22 AAB/76958 1049.5 84.8 237 21 AAY96289 1043.5 84.4 241 22 AAB/76289 1043.5 84.4 241 22 AAB/8212 1043.5 84.9 237 21 AAY96301 1058 83.8 234 18 AAW11638 1021 82.5 237 20 AAW/3873 1021 82.5 237 20 AAW/3873 1019 82.4 236 16 AAR77614  AAGG-2000 (first entry) anised anti-ras designed light chain Leu 2 protein. ; antibody; human; anti-inflammatory; anti-anemic; antibody; human; anti-inflammatory; anti-anemic; antioned arthritis; gradic lupus ery himoto disease; hymomophemia; departure syndrome; crohn's disease; thrombopenia pulin dependent diabetes mellitus; arteriosclerosis; thetic.	32	1070		218	22	AAB76949	Full length light
1070 86.5 218 22 AAB76588 1040.5 84.8 237 21 AAR96588 1040.5 84.8 237 21 AAR96289 1040.5 84.8 237 21 AAR96289 1041.5 84.4 24 122 AAB82912 1041.5 84.4 24 12 AAR83162 1041.5 84.9 237 21 AAR96301 1037.5 83.9 237 21 AAR96301 1038 83.8 234 18 AAW11638 1021 82.5 237 20 AAW73873 1019 82.4 236 16 AAR77614  ALIGNMENTS  ALIGNMENTS  AUG-2000 (first entry) anised anti-fas designed light chain Leu 2 protein.; antibody; human; anti-inflammatory; anti-anemic; antibody; human; anti-inflammatory anti-anemic; antibody; human; anti-inflammatory anti-anemic; antibody; human; anti-inflammatory anti-anemic; antionfertility; neuroprotective; antiantoropic; anti-arthritic; antivitis; systemic lupus ery himoto disease; rhemmatoid arthritis; graft versus rignor's syndrome; anemia; Addison's disease; thrombopenia pulp esclerosis; Basedow's disease; transpoliting expendent diabetes mellitus; arteriosclerosis; thetic.	ω e ω e	1070		218	7 7	AAB/6951	Full length light Variable light cha
1049; 8 84.8 237 21 AAY96298 1045.5 84.8 237 21 AAY96298 1046.5 84.4 240 20 AAA80161 1046.5 84.4 241 22 AAB82912 1041.5 84.2 234 14 AAR8162 1037:5 83.9 234 14 AAR81638 1023 82.7 240 22 AAG5665 1023 82.7 240 22 AAG5665 1021 82.5 237 20 AAW73873 1019 82.4 236 16 AAR77614  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  anised anti-Fas designed light chain Leu 2 protein. ; antibody; human; anti-inflammatory; anti-anemic; i-allergic; anti-arthritic; antiviral; immunomodula matological; immunosuppressive; thyromimetic; antivorce; antiar atotropic; humanized; apoptosis; systemic lupus ery humco disease; rhematold arthritis; graft versus rights exlearose; anematological; anematologica	٠ د د	1070		218	2 2	AAB76958	Variable light cha
1048 84.7 240 20 AAY50161 1045.5 84.5 237 21 AAY96289 1043.5 84.4 241 22 AAB82012 1041.5 84.2 234 14 AAR38162 1037.5 83.9 234 14 AAR38163 1038 82.7 240 22 AAG63665 1021 82.5 237 20 AAW73873 1021 82.5 237 20 AAW73873 1019 82.4 236 16 AAR77614  ALIGNMENTS  **ALIGNMENTS**	36	. 2		237	21	AAY96298	Human IGFAM-10 imm
1043.5 84.5 237 21 AAR96289	37	1048		240	20	AAY50161	Human reshaped F19
1043.5 84.4 241 22 AAB812912 Human namn 1041.5 84.4 241 14 AAR38162 Human in 1mm 1041.5 84.2 234 14 AAR38162 Human ant 1036 83.9 237 21 AAY96301 Human ant 1026 83.8 234 18 AAW11638 Human ant 1021 82.5 237 20 AAW3873 Human anti 1021 82.5 237 20 AAW787514 Human anti 1019 82.4 236 16 AAR77614 Human anti 1019 82.4 236 16 AAR77614 Human anti 1019 82.4 236 16 AAR77614 AUGNENTS  ALIGNMENTS  ALI	38	1045.5		237	71	AAY96289	IGFAM-1
1037.5 84.2 234 14 AARY88102 Sequence of 1036 83.8 234 18 AAR11638 Human Information 1023 82.7 24 0.2 AAR68365 Amino acid 1023 82.7 24 0.2 AAR68365 Amino acid 1021 82.5 236 16 AAR77614 Human intification 1019 82.4 236 16 AAR77614 Human ised Human antification 1019 82.4 236 16 AAR77614  ALIGNMENTS  ALIGNME	930	1043.5		241	22	AAB82912	Human immune respo
1031 3 33 3 23 4 14 AAN11638 Human antional 1023 82.7 240 22 AAG5365 Amino actional 82.5 237 20 AAW73873 Human antional 1019 82.4 236 16 AAR77614 Human antional 82.5 237 20 AAW73873 Human antional 82.4 236 16 AAR77614  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  AG5-2000 (first entry)  anised anti-Fas designed light chain Leu 2 protein.  antibody; human; anti-inflammatory; anti-anemic; antidiabeti matological; immunosuppressive; hyromimetic; antinfartendoscler; antional actional actional actional approasa; systemic lupus erythematosus; himocoupics; nemmatold arthritis; arthritis; antiarterioscleric attoropic; humanized; apoptosis; systemic lupus erythematosus; himocoupics antinfartulity; neuroprotective; antiarterioscleric attoropic; numanized; apoptosis; systemic lupus erythematosus; himocoupics and antiarterioscleric attoropic; numanized; apoptosis; systemic lupus erythematosus; himocoupics and actional actional actional appearure syndrome; crohn's disease; sterility; myasthenia gravutible sclerosis; Basedow's disease; thrombopenia purpura; alle diomyopathy; glomerulonephritis; hepatitis; transplant rejectithetic.	40	1041.5		234	T 4	AAR38162	the
1023 82.7 240 22 AAGGSGS AMINO COLORS AMINO COLORS B2.5 237 20 AAM73873 Human anti 1019 82.4 236 16 AAR77614 Human anti 1019 82.4 236 16 AAR77614 Human anti 1019 82.4 236 16 AAR77614 Human anti 109031 standard; Protein; 238 AA.  90931 standard; Protein; 238 AA.  90931; AuG-2000 (first entry)  anised anti-Fas designed light chain Leu 2 protein.  anised anti-Fas designed light chain Leu 2 protein.  anised anti-Farthitic; antiviral; immunomodulatory; cardi marologics, immunosuppressive; thyromimetic; antiartenmentic; antiviral; immunosuppressive; thyromimetic; antiartenmentosis systemic lupus erythematosus; himoto disease; rheumatoid arthritis; graft versus host disease; sterility; myasthenia gravitgen's syndrome; crohn's disease; sterility; myasthenia gravitin dependent diabetes mellitus; arteriosclerosis; myocarditi diomyopathy; glomerulonephritis; hepatitis; transplant rejectithetic.	4 1	1036		23/	181	AAY 90 3 0 1 AAW 11638	anti-RSV
101 82.5 237 20 AAN73873 Human anti 1019 82.4 236 16 AAR77614 Human anti 1019 82.4 236 16 AAR77614 Humanised Humanised 20931 standard; Protein; 238 AA.  90931; AuG-2000 (first entry) anised anti-Fas designed light chain Leu 2 protein.  3 antibody; human; anti-inflammatory; anti-anemic; antidiabeti i-allergic; anti-arthritic; antiviral; immunomodulatory; cardi matological; immunosuppressive; hypomimetic; antiarteroscleratoropic; antimefertulity; neuroprotective; antiarteroscleratoropic; appearure syndrome; anemia; systemic lupus erythematosus; himoto disease; rheumatoid arthritis; graaf versus host disease; sclerodern stellity myasthenia gravitipe sclerosis; Basedow's disease; thrombopenia purpura; alleulin dependent diabetes mellitus; arteriosclerosis; myocardii dinnique dinnique alleus; transplant rejectithetic.	4 4	1023	82.7	240	22	AAG63665	acic
ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  1 190931 standard; Protein; 238 AA.  900931;  AUG-2000 (first entry)  anised anti-Fas designed light chain Leu 2 protein.  1 antibody; human; anti-inflammatory; anti-anemic; antidiabeti  1 allergic; arti-arthritic; artiviral; immunomodulatory; cardi  matological; immunosuppressive; thyromimetic; antiarterboscler  attorropic; antiinfertility; neuroprotective; antiarterboscler  attorropic; antiinfertility; neuroprotective; antiarterboscler  attorropic; antimination atthritis; graft versus host disease; himnot disease; rheumatoid arthritis; systemic lupus erythematosus; himnot disease; rheumatoid arthritis; systemic lupus erythematosus; himnot disease; scherostis; myasthenia graft appasture syndrome; or phn's disease; thrombopenia purpura; alle ulin dependent diabetes mellitus; arteriosclerosis; myocarditi diomyopathy; glomerulonephritis; hepatitis; transplant reject thetic.	44	1021		237	20	AAW73873	anti
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190931 standar 190931; AUG-2000 (fi anised anti-F; antibody; h 1-allergic; a matological; himotological; himoto diseas rigen's syndro dpasture synd tiple scleros tiple scleros diomyopathy; thetic.						ALIGNMENTS	
90931 standar 90931; AUG-2000 (fi anised anti-F i antibody; h i-allergic; a matological; matoropic; an atotropic; an atotropic; an atotropic; an atotropic; an timent synd diensorate synd tiple soleros diensopath; asynd tiple soleros diensopath; tiple soleros diensopath;	SULT						
AAW90931;  08-AUG-2000 (first entry)  Humanised anti-Fas designed light chain Leu 2 protein.  Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; hyromimetic; antirhematic; anti-relammatic; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatorid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; soleroderma; sterility; Goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocardiis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	AA	90931	tandard;	Prote		œ	
Humanised anti-Fas designed light chain Leu 2 protein.  Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; hyromimetic; antirhematic; anti-relargic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; hemmia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocardiis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	AA	W90931;					
Humanised anti-Fas designed light chain Leu 2 protein.  Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; hyromimetic; antirhematic; anti-reliant lepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addiseon's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Synthetic.	Ċ	000			1		
Humanised anti-Fas designed light chain Leu 2 protein.  Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotropic; antininfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	80	-Aug-200			ξ.		
Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; hyromimmetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; nemmia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpurs; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	Hu		anti-Fas	desig		chain Leu	
anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimmetic; antirhemmatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; nemnia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Synthetic.	F.	s: antib	odv: him	מה: מה	t.i - i	nflammatory: ant	i-anemic: antidiabetic:
dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	KW an	ti-aller	qic; ant	i-arth	riti	c; antiviral; im	munomodulatory; cardiant;
nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic, humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; nemmia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Synthetic.	de	rmatolog	ical; im	nsounm	ppre	ssive; thyromime	tic; antirheumatic; anti-Fas;
5- ·-	ne	phrotrop	ic; anti	infert	1111	y; neuroprotecti	ve; antiarteriosclerotic;
>	he:	patotrop	ic; huma	nized;	apo	ptosis; systemic	lupus erythematosus;
>- ·-	Ha	shimoto	disease;	rheum	atoi	d arthritis; gra	
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insulin dependent diabetes mellitus; arterioscierosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Synthetic.	8 8	ltiple s	clerosis	Base	down,	s disease: throm	hopenia purpura: allerdy:
glomerulonephritis; hepatitis; transpla	i.	sulin de	pendent	diabet	es	ellitus; arterio	sclerosis; myocarditis;
Synthetic.	Ca	rdiomyop	athy; gl	omerul	onep	ritis;	transpla
	Sy	nthetic.					

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cells with an abnormal Fas/Fas apoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between canti-anematic antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirhetmatic, nephrotropic, antilnfertility, neuroprotective, contiarterioscleroric, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent disease associated with the Fas/Fas ligand system, especially systemic capportosis by binding to cell surface Fas or inhibit it by competitive constructions of system, cooppasture syndrome. Collescase, solutional system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin capponent diabetes mellitus, allergy, arterioscielerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic collucting a human anti-murine antibody response. This sequence represents a human set in the method of the invention.
                                                                                                                                                                New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                               Takahashi T;
                            Tamaki I,
                            Nakahara K,
                                                                                                                                                                                                                                                                          Claim 2; Page 159; 263pp; English.
                            Haruyama H,
                                                                                WPI; 2000-258930/23
                                                                                                               N-PSDB; AAA11632
                            Serizawa N,
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Gaps Length 238; Indels DB 21; 100.0%; Score 1237; DB 21 100.0%; Pred. No. 4.1e-60; tive 0; Mismatches 0; Best Local Similarity 100. Matches 238; Conservative Query Match ö

238 AA;

Sequence

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9 1 METDTILLMVLLLMVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY

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61 61 ò g

TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 121 à 셤

181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 õ

AAW90930 standard; Protein; 238 AA. RESULT AAW90930

AAW90930;

08-AUG-2000 (first entry) NX X

Humanised anti-Fas designed light chain Leu 1 protein.

anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; mephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

Synthetic.

EP990663-A2.

05-APR-2000

99EP-0307711. 29-SEP-1999; 98JP-0276881. 98JP-0276882 30-SEP-1998; 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Takahashi T; Serizawa N, Haruyama H, Nakahara K, Tamaki I,

2000-258930/23. N-PSDB; AAA11631

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 3; Page 156-157; 263pp; English.

This invention describes a nove inumarized anti-ras and prevents apoptosis in cells with an abnormal Fas/Fas inqueucle (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents core apoptosis in cells with a normal system, by inhibiting binding between fas and its ligand. The products of the invention have anti-inflammatory, anti-anamic, antidiabetic, anti-alergic, anti-arthritic, antivital, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antimicertility, neuroprotective, antirheumatic, associated with the Fas/Fas ligand system, especially systemic inhibition of ligand binding. (I) are used to treat and/or prevent diseases, slorgent system, especially systemic versus host disease, soleroderma, Goodpasture synthemia gravis, disease, autoinmune hemolytic anemia, Goodpasture synthemia gravis, anemia, Addison's disease, thrombopeania purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human anti-main and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic a human anti-murine antibody light chain construct designated beut a humanised anti-was antibody light chain construct designated beut a humanised anti-reas antibody light chain construct designated beut a humanised anti-reas antibody light characteries. This invention describes a novel humanized anti-Fas antibody-like

238 AA; Sequence

Gaps 0; Length 238; Indels Score 1233; DB 21; Pred. No. 6.7e-60; ö ; Pred. No. 6.7e 99.78; 99.68; Matches 237; Conservative Similarity Query Match Best Local 9

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1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60

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anti-allergic; anti-arthritic; antiviral; immunomodulatory cardiant; demachological; immunosupressive; thyrominetic; antiheumatic; anti-Fras; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashumcto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; untilpie sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardlomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                         QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                              121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                  GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised anti-Fas designed light chain Leu 3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 161-162; 263pp; English.
                                                                                                                                                                                                                                                                                                                                         AAW90932 standard; Protein; 238 AA
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98JP-0276882.
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lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively influit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-marsh antibody light chain construct designated Leu 3 which is described in the method of the invention.
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associated with the Fas/Fas ligand system, especially systemic
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis; HFE7A, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AlDS;
                                                                                                                                                                                                                                                                                                                                                                      Length 238;
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Pred. No. 7.6e-60;
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21..38
/label= Mat_protein
21..131
/label= Variable
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                                                                                                                                                                                                                                                                                                                                                                  99.68;
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Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                238 AA;
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chain of murino acid sequence or the PDHH type humanised light chain of murino acid sequence (see AAW83042) entailed making DIE, P47A, K49F, H805, P81R, V82L, B84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coll plants SANK 7039B harbors plasmid pHSHF2 carrying a fusion fragment of the humanised PDHH type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Heshimoto's disease, cliencederma, Goodpasture syndrome, Croin's disease, rheumatoid arthritis, autoimmune haemolytic anamia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, atopy, arteriosclerosis, modelis, ABDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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Tohru T;
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Masahiko O, Nobufusa S, Shin Y,
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/label= CDR_L1
/note= "claim 9"
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113..121
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/note= "claim 9"
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N-PSDB; AAV70077.
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25-JUN-1997;
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       DB 19; Length 238;
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Query Match 95.1%; Score 1177; DB 19; Best Local Similarity 93.3%; Pred. No. 7.2e-57; Matches 222; Conservative 9; Mismatches 7;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy. glomerulonephritis, aplastic anaemia (panmyolophthisis), hepatitis AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
                   QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                          121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                    181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                        Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody light chain, SEQ ID NO:107.
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Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
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                                                                                                                                                     QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                       TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                      181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                        Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                  METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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7.2e-57;
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                                Mismatches
                Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                          AAW90927 standard; Protein; 238 AA.
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              93.38;
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antirheumatic, nephrotropic, antilnfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus errythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Siorgen's syndrome, perntcious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoinmune hemolytic anemia, sterility, mysathenia gravis,
antiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
munanised anti-Fas antibody HRE7A designed light chain which is used in
the method described in the invention.
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Pred. No. 7.2e-57;
9; Mismatches 7; Indels 0;
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93.3%;
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Best Local Similarity
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Claim 21; Page 199-199; 292pp; English.
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                                      /note= "claim 9"
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                                                              /label= CDR_L3
/note= "claim 9"
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/label- CDR_L2
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/label= CDR_L1
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                                                                                                                                          Masahiko O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sjogren syndrome, pernicious anaemia, Addison's disease, relemanted scletoderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, anayocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of the HH type humanised light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leyuk1 H, Hiroko Y, Jun O, Kimihisa I;
Nobufusa S, Shin Y, Tohru T;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, atterioscierosis, myocarditis, cardiomyopathy, glomerulonephiritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and AABB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; carditomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                           QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                         9
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                                                                                                                                                                                                                      181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                       METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                     Humanised anti-Fas antibody light chain, SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 78-79; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                AAB14772 standard; Protein; 238 AA
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Chimeric - Homo sapiens.
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238 AA;

Sequence

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Gaps

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Length 238; Indels

94.7%; Score 1172; DB 19; 92.9%; Pred. No. 1.3e-56; Live 9; Mismatches 8;

Conservative

Matches 221;

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Query Match Best Local 8

Similarity

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                                                                                                                                                                                                                                                                                                                                                                 Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; anti-remnatic; anti-res; nephrotropic, antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; unultiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                                     QOKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                       Gaps
                                                                          METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                           GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis selectively
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                                                                                                                                                                                                                                                                                                                                              Humanised anti-Fas antibody HFE7A light chain HH type protein.
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                       Length 238;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example reference 14; Page 114-115; 263pp; English.
                       DB 21;
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&
                   Score 1172; DB 21
Pred. No. 1.3e-56;
9; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells with abnormal Fas-Fas ligand systems
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                    94.78;
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                         (first entry)
                              Similarity 92.9
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haruyama H,
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                                          221;
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                    Query Match
Best Local 9
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                                        Matches
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disease, autoimmune hemolytic anemia, sterility, mysathenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, mycarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mind the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFETA light chain HH type which is used in the method described in the invention.
   of the invention have anti-inflammatory,
Fas and its ligand. The products of the invention have anti-inflammatory anti-anemic, antidiabetic, anti-allergic, anti-archritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1172; DB 21; Length 238;
Pred. No. 1.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atopy; arteriosclerosis; myocarditis; cardiomyopathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 92.9
Matches 221; Conservative
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Synthetic

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Length 238;

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...20
'label- Sig_peptide
             21..238
/label- Mat_protein
Location/Qualifiers
                                                                                                                                                                                                            Claim 21; Page 200; 292pp; English.
                        11.131
'label= Variable
                                 132..238
/label= Constant
                                                                    /note= "claim 9"
                                                     'note- "claim 9"
                                                                                  /note= "claim 9"
                                            44..58
/label- CDR_L1
                                                          74..80
/label- CDR_L2
                                                                        113..121
/label= CDR_L3
                                                                                                               98AU-0059701.
                                                                                                                         97JP-0276064
                                                                                                                             97JP-0082953
97JP-0169088
                                                                                                                                                                                                                                                                                                                                            rejection (all claimed).
                                                                                                                                            (SANY ) SANKYO CO LID.
                                                                                                                                                      Hideyuki H,
                                                                                                                                                                    WPI; 1998-543440/47.
                                                                                                                                                                                                                                                                                                                                                      238 AA;
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                                                                                                                              01-APR-1997;
25-JUN-1997;
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Key
Peptide
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              Protein
                        Region
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This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entabled making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coli pisGAHM1 SANK 7397 harbors plasmid pHSGHM1 carrying a fusion fragment of the humanised HW type HEF7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is encoding the region of human immunoglobulin kappa chain, and is encoding the region of human immunoglobulin kappa chain, and is encoding the region of human immunoglobulin kappa chain, and is encoding the region of human ised antibodies by culturing host cells. Humanised versions of HFF7A (see AAW83031-37), like native expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal colls. The humanised antibodies are used to evaluate, in animal interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, Addison's disease, Slogren syndrome, pernicious anaemia, Addison's disease, sleroderma, Goodpasture syndrome, Crohn's disease, thrombopenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, mycozaditis, cardiomyopathy, glomerular chepticis, hypoplastic anaemia, hepatitis, AlbS and transplant references.
                                                                                                                                                                                                                                                                                                                                                New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
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(complementarity determining regions) to antibody HEE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-194778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE/A, or a humanised version of HFE/A containing identical CDRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \int
                                                                                                                                                                                                                                                                                                                                                                                QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                   1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised anti-Fas antibody light chain, SEQ ID NO:52.
93.7%; Score 1159; DB 19; 92.0%; Pred. No. 6.8e-56;
                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 80-81; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB14773 standard; Protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0276883.
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                                                                                              Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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N-PSDB; AAA72125.
    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; anti-rematic; anti-res; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                  TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                            QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                         Gaps
                                                                                                        1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                 Humanised anti-Fas antibody HFE7A light chain HM type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakahara K, Tamaki I, Takahashi T;
                                                    Length 238;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example reference 14; Page 117-118; 263pp; English.
                                                    DB 21;
                                                  Score 1159; DB 21;
Pred. No. 6.8e-56;
); Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                   AAW90923 standard; Protein; 238 AA.
                                                  93.7%; Sco
92.0%; Pre
live 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0276881.
98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haruyama H,
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N-PSDB; AAA11563.
                                                              Similarity
                    238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                            08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP990663-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2000
                                                                       Matches 219;
 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                      AAW90923;
                    Sequence
                                                   Query Match
                                                              Best Local
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molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antilnfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit if by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatold arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autolimune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephitis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEFA light chain HM type which is used in the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Fas humanised antibody HFE7A light chain PDHM type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.08;
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Best Local Similarity
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238 AA;

Sequence

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Gaps

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This is the amino acid sequence of the PDHM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these crastions acid in phship chain. Host cell Escherichia coll phship SARK 7019B harbors plasmid phSHM2 carying a fusion of the humanised PDHM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, classes, soleroderma, Goodpasture syndrome, Croin's disease, theumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, hipsoplastic anaemia, hepatitis, hipsoplastic anaemia, hepatitis, hypoplastic anaemia, hepatitis, and propersula purpura and insulan-dependent diabetes) allergies, atopy, arteriosclerosis, models cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, hypoplastic anaemia, hepatitis, and propersular and insulan-dependent diabetes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 220-221; 292pp; English.
                                                                                          /label= Sig_peptide
21.238
/label= Mat_protein
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                      74..80
/label= CDR_L2
/note= "claim 9"
                                                                                                                                                                                                                                                                                                                                            /"CCE CIGIN 9
113..121
/label CDR_L3
/note= "claim 9"
                                                                                                                                                    11.131
/label= Variable
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/label= Constant
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/label- CDR_L1
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Masahiko O, Nobufusa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-543440/47.
N-PSDB; AAV70078.
  Homo sapiens.
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25-JUN-1997;
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                  Synthetic.
                                                                          Peptide
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                      61 QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                         121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                               1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                             181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                               Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised anti-Fas antibody light chain, SEQ ID NO:109.
Score 1158; DB 19;
Pred. No. 7.7e-56;
 93.6%; Score 92.0%; Pred. No. /...
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAB14778 standard; Protein; 238 AA.
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            Query Match
Best Local Similarity 92.09
Matches 219; Conservative
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Chimeric - Homo sapiens.
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N-PSDB; AAA72177.
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 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                          OOKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                     121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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Pred. No. 7.7e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised HFE7A designed light chain protein #2.
                                                                                                                                                  10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90928 standard; Protein; 238 AA.
                                                                                                                       93.6%;
92.0%;
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                                                                                                                      Query Match 93.6
Best Local Similarity 92.0
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-258930/23.
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30-SEP-1998;
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Search completed: August 14, 2002, 15:15:35 Job time: 833 sec

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This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas concluded by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between the proposition of the invention have anti-inflammatory, anti-anemic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antiviral, immunosuppressive, thyromimetic, continuateriosclerotic, antiinfertility, neuroprotective, antiinfermatic, antininfertility, neuroprotective, antiinfermatic, antiviral, immunosuppressive, thyromimetic, continuateriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent contens host disease associated with the Fas/Fas ligand system, especially systemic upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft correspondent diabetes molificants of alsease, soleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic, and transplant rejection. (I) selectively conthine disease models (I) act on the active site of Fas, i.e. they mimic cells. They bind to both human and murine Fas, so can be evaluated in curine disease models. (I) act on the active site of Fas, i.e. they mimic inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody response. This sequence represents the method described in the invention.
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Example reference 21; Page 144-145; 263pp; English.
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10; Mismatches
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Best Local Similarity 92.0°
Matches 219; Conservative
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2, Appli 40, Appli 6, Appli 10, Appli 2, Appli 2, Appli 62, Appli 62, Appli 51, Appli

Sequence

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APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1108; DB 5;
Pred. No. 1.6e-87;
US-08-788-800-11

US-08-437-6428-40

US-09-097-309-2

US-09-097-171A-2

US-09-097-339-6

US-09-097-712B-2

US-09-097-712B-2

US-09-027-712B-2

US-09-027-712B-2

US-09-027-49-62

US-09-027-449-51

US-08-027-444-51

US-08-026-985-51

US-09-027-444-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

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US-09-026-985-72

US-09-026-985-72
                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9613152 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Ha
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-Sep-95
ATTORNEY/AGENET INFORMATION:
NAME: NOTMAN D. HANGON
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
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97.78;
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Best Local Similarity
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RESULT
                                                                       August 14, 2002, 15:17:03 ; Search time 82.88 Seconds (without alignments) 70.141 Million cell updates/sec
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                                                                                                                                      1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
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Compugen Ltd
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US-09-109-207C-13
US-09-296-005-13
US-09-286-163B-9
US-09-282-505-1
US-09-054-255-1
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US-09-109-207C-19
US-09-296-005-15
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US-09-296-005-19
US-09-296-005-19
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US-08-437-642B-25
PCT-US93-07832-25
US-07-934-373C-39
PCT-US93-07832-39
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US-08-887-352B-17
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            GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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length: 2000000000
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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                                DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
                                                                                                  81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1096; DB 2;
Pred. No. 1.7e-86;
                                                                                                                                                                                                                                                             201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9001
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
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97.2%;
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 Conservative
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Best Local Similarity 97.2
Matches 212; Conservative
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213;
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Matches
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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Pred. No. 1.7e-86;
3; Mismatches 3;
                         181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
CITY: South San Francisco
COUNTRY: USA
ZIE: 94080
COMPUTER REPABLIE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/466,151 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGRAT INFORMATION:
                                                                                                                                               Sequence 9, Application US/08466151 Patent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                 Genentech, Inc.
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Best Local Similarity 97.2%;
Matches 212; Conservative 3
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                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                               US-08-466-151-9
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                                                                                                                                                                                                                                                                                                                                                                                       81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                          Length 218;
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; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: humanized maell, version 1, light chain US-08-466-1638-9
                                                                                                          Score 1096; DB 4; Length 2
Pred. No. 1.7e-86;
3; Mismatches 3; Indels
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88.6%; Score 1096; DB 4;
Best Local Similarity 97.2%; Pred. No. 1.7e-86;
Matches 212; Conservative 3; Mismatches 3;
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Patent No. 6329509
GENERAL INPORMATION:
APPLICANT: Jardideu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION UNMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1995-05-07
PRIOR FILING DATE: 1992-05-07
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                                                                                                          Query Match
Best Local Similarity 97.2%;
Matches 212; Conservative
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US-08-466-163B-9
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Patent No. 6290957
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123GLT
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                              APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REPERBUCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 13
LENGTH: 218
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        IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                            GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-109-207C-13
                                                                                    STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                  Sequence 13, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial FEATURE: NAME/KEY: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Artificial LOCATION: 1-218
                                                                                                                                                                                                                US-09-109-207C-13
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCE: 26
CORRESPONDENCE ADDRESS:
                                       81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                   IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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                                                                                                                                                                                             201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/887,352B
                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-Jul 1997
CLASSIFICATION: 530
ATTORES/AGENT INPORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STAATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 amino acids
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Best Local Similarity 95.0%
Matches 207; Conservative
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US-08-887-352B-15
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Pred. No. 1.6e-84;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 1-218
. OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: E27 anti-IgE antibody light chain US-09-054-255-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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Patent No. 6242195;
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptide Variants;
FILE REFERENCE: P1266;
CURRENT APPLICATION NUMBER: US/09/054,255;
CURRENT FILING DATE: 1998-04-02
                                                                                                                             GENERAL INFORMATION:
APPLICANT: ESOBE Ekinaduese Idusogie et al.
TITLE OF INVENTION: POLYDEPLIGE VARIANTS
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 10
                                                                                           Sequence 1, Application US/09282505A
Patent No. 6194551
                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 95.4%;
Matches 208; Conservative
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Matches 208;
                                                     RESULT 7
US-09-282-505-1
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US-08-887-3528-24

Sequence 24, Application US/08887352B

Sequence 24, Application US/08887352B

Patent No. 5994511

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
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Pred. No. 2.9e-84;
6; Mismatches 5;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPATIBLE
SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Winderin (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-7u1-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFRENCE/CDOCKET NUMBER: 91123
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 10 NFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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95.0%;
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: 218 amino acids
Amino Acid
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Best Local Similarity 95.09
Matches 207; Conservative
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   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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TOPOLOGY:
US-08-887-352B-19
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                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                         APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STREET: California
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Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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Pred. No. 2.9e-84;
6; Mismatches 5
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELEPHONE: 650/225-1489
TELEPHONE: 650/952-9881
                                                                                                                                                      Sequence 17, Application US/08887352B Patent No. 5994511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08887352B Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonan ITITLE OF INVENTION: Improved Anti-TITLE OF INVENTION: Improving PolyNUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TENGTH: 218 amino acids
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95.0%;
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US-08-887-352B-17
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept FILE REPERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
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US-09-109-207C-19
US-09-109-207C-19
Sequence 19, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
TILLE REPREMENCE: PILL3R
TILLE REPREMENCE: PILL3R
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT APPLICATION NUMBER: US 60/051,554
PRIOR APPLICATION NUMBER: US 60/051,554
NUMBER OF SEQ ID NOS: 44
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                           61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYXCQQSHEDPYTFGGGTKVEIKRTVAAPSVF 120
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95.0%; Pred. No. 2.9e-84;
iive 6; Mismatches 5;
                                                                                                                                                                                                                                    201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Matches 207; Conservative
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SEQ ID NO 17
LENGTH: 218
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US-09-109-207C-17
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LENGTH: 218
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Patent No. 6172213
GENERAL INFORMATION:
GENERAL FILING DATE:
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COTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15
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Pred. No. 2.9e-84;
6; Mismatches 5;
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Pred. No. 2.9e-84;
6; Mismatches 5;
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.....ER: US/08/887,352B
.03-Jul-1997
.08: 530
IMPG
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFRENCE/DOCKET NUMBER: P112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
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95.0%;
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95.0%;
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                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear
US-08-887-3528-24
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Matches 207; Conserv
                                                                                                               CLASSIFICATION:
                                                                                FILING DATE:
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US-09-109-207C-15
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) ORGANISM: Artificial
FEATURE:
NAME/KE: Artificial
LOCATION: 1-218
OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19
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                                                                                                             Query Match

86.5%; Score 1070; DB 4; Length 218;

Best Local Similarity 95.0%; Pred. No. 2.9e-84;

Matches 207; Conservative 6; Mismatches 5; Indels
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62DX
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ig kappa chain NIG	Iq kappa chain NIG	kappa chain	kappa chain	kappa chain	Ig kappa chain pre	Ig kappa chain V r	kappa	Ig kappa chain pre	monoclonal antibod	kappa ch		kappa chain	kappa		kappa	kappa			kappa	kappa			kappa chain		kappa	kappa chain	lambda-like	appa
SUMMARIES	ID	JE0242	JE0244	JE0243	A23746	JE0241	S06084	S68241	S33161	S14237	JC5810	A31790	S01320	A56169	537484	PC4203	S52028	S38865	S25058	S68212	S42772	S16112	JL0029	A20969	PT0219	S52059	S29593	PH1226	A49633	PL0106
	Length DB	215	'n	ъ	'n	9	0	m	0	₩.	ഹ	220 2	₹	0	'n	on.	0	<u>о</u>	'n	₹	_	a	'n	on.	m	'n	_	_	m	-
ф	Query Match	76.8	75.2	73.4	71.9	71.2	65.7	6.09	8.09	8.09	60.7	59.0	58.6	58.4	58.2	57.7	57.2	57.1	57.1	26.7	56.4	55.9	55.0	49.9	49.5	49.2	47.4	47.1	46.3	44.5
	Score	949.5	930.5	907.5	889.5	881	813	753	752.5	752	751	730	725	722	720.5	713.5	707.5	706.5	706.5	701	697.5	691.5	680.5	617.5	612	608.5	586.5	583	572.5	551
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30 548 44.3 106 1 31 536 44.3 131 1 32 521 42.1 132 1 33 520 42.0 233 2 34 518 41.9 123 2 35 514 41.9 123 2 36 514 41.6 141 2 37 513 41.5 99 2 38 509.5 41.2 146 2 40 507 41.0 0 40 507 41.0 0 40 40.4 122 2 44 499 40.3 132 2 44 499 40.3 132 2 45 503 40.7 131 2 47 600 40.4 122 2 48 600 40.4 122 2 49 600 40.4 122 2 49 600 40.4 122 2 49 600 40.4 122 2 49 600 40.4 122 2 49 600 40.4 122 3 40 600 600 600 600 600 600 600 600 600 6	KXMSM6 KVMSM6 KVMSM6 S29577 S40331 A49134 A37927 A49134 A37927 S40365 S40368 S40368	human vision n, M.S. 8 nship o nship o nclogy score pred. 14; Mi cRASGSV CRASGSV QPEDFAT       EPEEFRAK FYPREAK FYPREAK FYPREAK	human vision M.S.; 8 k type region;
30 548 44.3 106 31 536 43.3 131 32 521 42.1 132 33 520 42.0 233 34 518 41.9 123 35 517 41.8 127 36 514 41.6 141 37 513 41.5 19 38 509.5 41.2 145 39 508 41.1 140 40 507 41.0 139 41 507 41.0 139 42 503 40.7 131 43 509.5 Homo sapiens (man) C; Species: Homo sapiens (man) C; Superfamily: immunoglobuli C; Superfamily: immunoglobuli C; Superfamily: immunoglobuli C; Superfamily: immunoglobuli D; Superfamily: immunoglobuli C; Superfamily: immunoglobuli C; Superfamily: immunoglobuli D; Species: Homo sapiens (man) C; Species: Homo sapiens	000000000000000	r - reg - re	- rei in, 1999
30 548 44.3 31 536 44.3 32 521 42.1 33 520 42.0 34 518 41.9 35 514 41.6 36 514 41.6 37 518 41.1 38 509.5 14 41.6 39 508 41.1 40 507 41.0 41 507 41.0 41 507 41.0 42 503 40.7 42 503 40.7 43 500 40.4 44 499 40.3 45 Accession: JED242 R;Alim, M.A.; Yamaki, Submitted to JIPID, NA. A;Description: JED242 R;Alim, M.A.; Iamaki, Submitted to JIPID, NA. A;Description: JED242 R;Alim, M.A.; Iamaki, Submitted to JIPID, NA. Best Local Similarit Matches 183; Consecond to JIPID, NA. C;Superfamily: immunog F;16-91/Domain: JBC244 F;20-10-10-10-10-10-10-10-10-10-10-10-10-10	1006 131 131 131 123 140 140 130 130 130 130 130 130	orecurso sequence S.; Hos vember III = 181 vember incompleted of the color of	ecursor is (man) equence; Hossa vember ubgroup 30243 sin
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Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                   71.9%;
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Matches 178; Conservative
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Matches 175; Conserv
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C;Species: Homo saplens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
C;Accession: JE0243
R;Alin, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; submitted to JIPID, November 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tily Kappa chain V-III (KAU cold agglutinin) - human C; Species: Homo sapiens (man) Species: Head of the species of the sp
                                                                                                                                                                                                                                                                                                                             140 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: A new subgroup of k type light chains (VkV) identified in A; Reference number: JE0243
A; Accession: JE0243
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                                                                              Score 930.5; DB 2;
Pred. No. 7.2e-54;
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Residues: 1-215 < ALIN.
C;Superfamily: immunoglobulin V region;
F;16-90/Domain: immunoglobulin homology
F;16-90/Domain: immunoglobulin homology
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83.6%;
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Best Local Similarity 82.29
Matches 180; Conservative
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JED2A1
R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JPPD. November 1998
A; Description: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: JED2A1
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                                                                                                                                                                                                                                                                                                                                                                                   119 IFPPSDEQLKSGTASYVCLLNNFYPREAKVQWKVDNALQSGNSQESYTEQDSKDSTYSLS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                          57
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                                                   homology
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A;Residues: 1-216 <ALL7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                      Length
                                                1mmunoglobulin
                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 881; DB 2;
Pred. No. 1.2e-50;
; Mismatches 27
                                                                                                                                                                   Score 889.5; DB 2
Pred. No. 3.3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
A.Molecule type: protein
A.Residues: 1-215 <LEO>
C.Superfamily: immunoglobulin V region; immuno
C.Reywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.2%; Score 881;
80.3%; Pred. No. 1.
ive 14; Mismatch
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a recombinant murine monoclonal antibod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1990
A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
A;Reference number: S33161
A;Accession: S33161
                                                                                                                                                                                                                                                                                                                                                              (domestic sheep)
#text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology <IMS-212/Domain: immunoglobulin homology <IMM>
         126 TKVEIKRTVAAPSVĖIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLWVLLLW-VPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:36-110/Domain: immunoglobulin homology <IMM>
                                                                           IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 230;
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                                                                                                                                                                                                                                                                                                                                                       C;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: S33161 R;Foley, R.C.; Beh, K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.8%; Sco...
62.7%; Pred. No. ...
...e. 35; Mismatches
                                                                                                                                                                   STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                             Score 752;
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Best Local Similarity 62.73
Matches 146; Conservative
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A;Molecule type: mRNA
A;Residues: 1-230 <FOL>
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                                                                                                                                                                                                                                                                                                                                   Ig kappa chain - sheep
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NyAlternate names: immunoglobulin light chain
C; Species: Mus musculus (house mouse)
C; Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: S68241; S68241
R; Takaqi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Immanka, T. submitted to the EMBL Data Library, March 1994
A; Reference number: S68241
A; Reference number: S68241
A; Rocession: S68241
A; Reference number: S68211; MUID: 9608523
A; Ritle: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin A; Reference number: S68211; MUID: 9608523
A; Rocession: S68244
A; References: EMBL: D29570
C; Superfamily: Immunoglobulin V region; Immunoglobulin homology
C; Reywords: Immunoglobulin
                                                   rat myeloma immunoglobulin kappa chain cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 PRIFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                  A.Accession: 506084
A.Molecule type: mRNA
A.Molecule type: mRNA
A.F.Molecule type: mRNA
A.F.Molecule type: mRNA
A.C.COSS-references: EMBL:X16129, NID:956457; PIDN:CAA34256.1; PID:956458
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin
F.1.20/Domain: signal sequence #status predicted <SIG>
F.1.240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGD--SYMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                        Score 813; DB 2; Length 24:
Pred. No. 3.6e-46;
"""matches 52; Indels
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Pred. No. 2.6e-42;
); Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                        65.7%; Sco...
65.0%; Pred. No. s...
ive 30; Mismatches
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3.
A:Reference number: S06084; MUID:90016888
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64.7%; Pre
tive 30;
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Matches 156; Conservative
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Best Local Similarity 64.77
Matches 141; Conservative
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Best Local Similarity
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Gaps

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Gaps

5;

Indels

49;

Score 730; DB 2; Pred. No. 8.3e-41;

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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C;Accession: S01320
R;de Maele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Bur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobuli A;Reference number: S01320; MUID:88329081
A;Accession: S01320
                                                                                                                                                                                                                                                                                                                                                                                                                      ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 198
                                                                                                                                                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDG--DSYMNWYQQKPGQAPKLLIYAASNL 78

    Y: immunoglobulin V region; immunoglobulin homology
heterotetramer; immunoglobulin

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.0%; Score 730; DB Best Local Similarity 62.3%; Pred. No. 8.3e Matches 137; Conservative 32; Mismatches
                               C; Keywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor - mouse
   C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A. Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr A;Reference number: JC5810; MUID:98063277
A;Accession: JC5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb_1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                        61 QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                             121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                    GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                       9
                                                                                                                                            1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTVTCKASQDI----NSYLSWI 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                                  4;
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels
Pred. No. 3.3e-42;
; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Pred. No. 3.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Mismatches
                            35;
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65.1%;
60.1%;
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Best Local Similarity 60.1
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-218 <AKA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: JC5810
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mouse recombinant immunoglobulin directe

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59 WYQQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNED 118
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A,Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-234/Product: Ig kappa chain #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                        1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMN--
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                                                                                                                                                                                                                                                                  Length 234;

    mouse (fragment)

                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                         58.6%; Score 725; DB 2; 57.9%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                               38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (clone 23.2) - C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.9%
Matches 139; Conservative
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1;

Gaps

1;

Length 219;

9

cDNAs coding for heavy and light chains

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A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-dersi
C;Superfamily: immunoglobulin v region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>
                                                                                         C.Species: Mus musculus (house mouse)
C.Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C.Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C.Accession: PC4203
R.KWAK, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIVLTQSPSSLSASVGDRVTITCKASQSVDY-DGDSYMNWYQQKPGQAPKLLIYAASNLE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
                                                                         Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.7%; Score 713.5; DB 2;
60.3%; Pred. No. 9.7e-40;
tive 36; Mismatches 50;
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ne: 687 sec
                                                                                                                                                                                                    A,Title: Cloning and characterization of c
A,Reference number: PC4202; MUID:97082978
A,Rocession: PC4203
A,Molecule type: mRNA
A,Residues: 1-219 <KWA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Matches 132;
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Job time:
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                                                      B.; Rosenbaum, H.; Godill
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C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000 C;Accession: A56169
R;Monfardini, C.; Réber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454
A;Accession: A56169; MUID:95204454
A;Accession: A56169 MUID:95204454
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: MRNA
A;Residues: 1-210 <ANN>
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain - mouse (fragment)
C.Species: Mis musculus (house mouse)
C.Species: Mis musculus (house mouse)
C.Species: Nis musculus (house mouse)
C.Accession: S37484
R.Pucancel, F.F.D.
A.Reference number: S37483
A.Reference number: S37483
A.Accession: S37484
A.Status: preliminary
A.Status: preliminary
A.Nolecule type: mRNA
A.Residues: 1-225 < DUC>
A.Cooss-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| ||: :||| ||:||| ||:|| |||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| LIXXASSRYTGVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQ-DYSSYTFGGGTKLEI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ 190
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                                                                                                                                                                                                                                                                                                             58.4%; Score 722; DB 2;
65.6%; Pred. No. 2.6e-40;
iive 27; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.2%; Score 720.5; DB 2 62.3%; Pred. No. 3.5e-40; ive 28; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STLTLSKADYEKHKVYACEVTHQGLSSPV 229
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Best Local Similarity 62.3
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 137;
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1 METDIILLWVLLLWVPGSTG......EVTHOGLSSPVTKSFNRGEC 238
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score		Match Length DB	B	CI	Description
1	548		106	Н	KAC_HUMAN	P01834 homo sar
7	536	43,3		Н	KV31_MOUSE	P01661 mus musc
3	521	42.1		Н	KV3F_MOUSE	P01658 mus musc
4	487	39.4		-	KV3M_MOUSE	P01665 mus musc
2	485	39.2		Н	KV3N_MOUSE	P01666 mus musc
9	483	39.0		Н	KV30_MOUSE	P01667 mus musc
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Des	P01	P01661	P01658	P01665	P01666	P01667	P18	P01	P04431	P01664	P01	P18136	P01600	P06314	P01605	P01599	P01603	P01594	P01597	P01598	P01606	P01660	P04430	P01593	P01602	P06313	P04207	P80362	P01607	P01662	P01608	P01663	P0161
8 ID	1 KAC_HUMAN	_	1 KV3F_MOUSE	_	_	1 KV3O_MOUSE	1 KV3L_HUMAN	1 KV3Q_MOUSE	1 KV1W_HUMAN	1 KV3L_MOUSE	1 KV3P_MOUSE	1 KV3M_HUMAN		1 KV4C_HUMAN	1 KV1M_HUMAN	1 KV1G_HUMAN	I KV1K_HUMAN	I KV1B_HUMAN	L KV1E_HUMAN	L KV1F_HUMAN	L KV1N_HUMAN	L KV3H_MOUSE					-		L KV10_HUMAN	L KV3J_MOUSE	L KV1P_HUMAN	L KV3K_MOUSE	KV1R_HUMAN
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Score	548	536	521	487	485	483	482.5	480	476	472	462.5	460.5	457	452	449	448	444	442	441	441	441	440	438	437	4	436.5	435.5	434	431	431	430	430	429
Result No.	п	7	3	4	S	9	7	8	6	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P06311 homo sapien P01670 mus musculu P01611 homo sapien P04432 homo sapien P01612 homo sapien P06310 homo sapien P01604 homo sapien P01671 mus musculu P01609 homo sapien P01695 mus musculu P01699 mus musculu	TrS	PRT; 106 AA. ed) sequence update) annotation update)	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	user U., Edelman G.M.; na G-immunoglobulin. VI. Amino	DISULFIDE BONDS. MEDLINE-71064027; PubMed-4923144; MEDLINE-71064027; PubMed-4923144; MEDLINE-71064027; PubMed-4923144;  "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";  Biochemistry 9:3188-3196(1970).	SEQUENCE (BENCE-JONES PROTEIN TI). MEDLINE-72188439; PubMed-5027703; Suter L., Barnikol H.U., Watanabe S., Hilschmann N.; Futle of antibody structure. The primary structure of a monoclonal immunoglobulin L-Chain of Kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete anino acid sequence and its significance for the mechanism of antibody production."; Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).	SEQUENCE FROM N.A. MEDLINE-81042304; PubMed-6775818; Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.; Hictoned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";	Langer B., Ponstingl H., 8.5.; on, pp.57-74, Academic Press,	Bence Jones protein Cum (kappa-
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4 429 6 426 6 425 7 421.5 9 420.5 0 420.1 1 418 3 415.5 5 416		1 MAN AC_HUMA 01834; 1-JUL-1 1-JUL-1 6-OCT-2 9 kappa	IGKC. Homo sapiens (Human) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TAXID=9606;	SEQUENCE (MYELONA PROTEIN EU). MEDLINE=71064023; PubMed=5489770; Gottlieb P.D., Cunningham B.A., Rutishauser U "The covalent structure of a human gamma G-imm acid sequence of the light chain.";	DISULFIDE BONDS. MEDLINE-71064027; PubMed-492314 Gall W.E., Edelman G.M.; "The covalent structure of a hu Intrachain disulfide bonds."; Biochemistry 9:3188-3196(1970).	131 SEQUENCE (BENCE- MEDLINE=72188439 Suter L., Barnik "Rule of antibod immunoglobulin L. Ti). IV. The com the mechanism of the mechanism of	SEQUENCE FRO MEDLINE-8104 Hieter P.A., "Cloned huma genes conser Cell 22:197-	CE etz ran ran glo ce	Hilschmann N.; "The complete type).";
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Matches 100;
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the disulfide bridges.";
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                                                                                                                                                                    Science 169:56-59(1970).
-1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER, 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 Kappa chain V.II region MOPC 63 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                          SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
MEDILINE-70201507; PubMed=5447531;
KOhler H., Shimizu A., Putnam E.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FIIGAVAR.003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

51984DIFDD372CE8 CRC64;
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
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                                              Fitani K., Shinoda T., Putnam F.W.;
The amino acid sequence of a kappa type
complete sequence and the location of the
J. Biol. Chem. 244:3550-3560(1969).
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                        SEQUENCE (BENCE-JONES PROTEIN AG).
MEDLINE-69234734; PubMed-4893682;
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InterPro; IPR003597; Ig_cl.
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SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
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106
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HSSP; P01842; 7FAB.
MIM; 147200; -.
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57
106 AA;
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MEDLINE-TYOU2520; PubMed-99744;
MCKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR, A01935; KWSM6.
HSP: P01789; LMCP.
InterPro: IPR003006; Ig_MRC.
InterPro: IPR003596; Ig_V.
Ffam: PF00047; ig; 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 sappa chain V-III region MOPC 321 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TAXID-10090;
                                                                                                                                                                                                                                                MEDIINE=73140225; PubMed=4691517; McKean D.J., Potter M., Hood L.E.; McKean D.J., Potter M., Hood L.E.; Mouse immunoglobulin chalns. Pattern of sequence variation among kappa chains with limited sequence differences."; Biochemistry 12:760-771(1973).
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               Burstein Y., Schechter I.;
"Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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MEDLINE=78235887; PubMed=98179;
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KV3N_MOUSE STANDARD; 1
P01666;
21-JUL-1986 (Rel. 01, Created)
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HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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                     diversity.";
Nature 276:785-790(1978).
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-!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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       SEQUENCE OF 1-37.
MEDLINE-7825887; pubMed-98179;
MEDLINE-78258887; pubMed-98179;
MEDLINE-7825887; Schechter I.;
"Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                                KAPPA CHAIN V-III REGION MOPC 321.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                             42.1%; Score 521; DB 1; Length 132; 68.2%; Pred. No. 4.7e-35; ive 27; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                                                                                                                                                                                                                14523 MW; 9F3B809BB773FBE9 CRC64;
                                                                                                                                                                                                                             Pfam; PF00047; 1g; 1. SMART; SM004067; 1g; 1. Immunoglobulin V region; Bence-Jones protein; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 7043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA.
                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
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                                                                                                SEQUENCE OF 21-132.
MEDLINE=73140224; PubMed=4120629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                PIR; A01933; KVMS32.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 68.2 tes 90; Conservative
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132
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73
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132
132 AA;
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[1]
SEQUENCE OF
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P01665;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 487; DB 1; Length 111;
Pred. No. 2e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12002 MW; 7A5FCB586C306D29 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7183.
Mas musculus (Mouse).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=79073152; PubMed=103003;
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sapiens (Human)
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                                                        21 DIVLTQSPSSLSASVGDRVIITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES 80
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Rearrangement of genetic information may produce immunoglobulin
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                                                                                81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                           61 GIPARFSGSGSGTDFTLNIHPVEEDDAATYYCQQSNEDPLTFGAGTKLELK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 483; DB 1; Length 111; Pred. No. 4.1e-32;
       Length 111;
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FRAMEWORK - 2.
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                           11; Indels
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       Score 485; DB 1;
Pred. No. 2.8e-32;
                                                                                                                                                         101667;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 6308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RV3L_HUMAN STANDARD; PRT; 129 AA. P18135; 01-NOV-1990 (Rel. 16, Created) LNOV-1990 (Rel. 16, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Ig kappa chain V-III region HAH precursor.
 39.2%; Scc...
81.1%; Pred. No. ...
10; Mismatches
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9; Mismatches
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PIR; C01937; KWMS08.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; I.
Immunoglobulin V region.
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81.1%;
                          90; Conservative
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                  Similarity
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KV30_MOUSE
ID KV30_MOUSE
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Best Local Si
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DT 15-JUL
DE IG KAPI
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61 QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Mutcantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i. DISBASE: THE PROPEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-III REGION HAH.
FRAMWOKK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMWOKK-2.
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COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
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14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.0%; Score 482.5; DB 1; ilarity 69.7%; Pred. No. 5.4e-32; Conservative 16; Mismatches 21;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region PC 7769.
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HSSP, POLT98; LINCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pram; PP00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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PIR; E01937; KVMS69.
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129
129 AA;
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Best Local Similarity
Matches 92; Conserv
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96;
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P01664;
                                                                                     Query Match
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                                                                                                                                                                                                                                   DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES 80
                                                                                                                                                                                                                                              1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKVLIFAASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85014148; PubMed-6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Walker precursor.
17 kappa chain V-I region Walker precursor.
18 kappa chain V-I region Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAPPA CHAIN V-I REGION WALKER.
                                                                                                                                                                                                                                                                          81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                                                                                                                                     38.8%; Score 480; DB 1; Length 111; 80.2%; Pred. No. 7.1e-32; Live 11; Mismatches 11; Indels
                                                                           COMPLEMENTARITY - DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                               COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                  COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                            6FAA345279356829 CRC64;
                                                                                                                                        SIMILARITY.
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FRAMEWORK-1
                                                                                                                              FRAMEWORK - 4
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PIR; A01883; KIHUWK.
HSSP, P01607, 1REI.
INTERPRO; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam, PF00A7; ig, 1.
Immunoglobulin V region; Signal.
SIGNAL
DOMAIN 23 129 IG KAPPA
DOMAIN 23 45 COMPLEMED
DOMAIN 46 56 COMPLEMED
DOMAIN 77 71 FRAMEWOR
                                                                                                                                                                                                                                                                                                                                                      PRT;
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
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111 AA;
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KV1W_HUMAN
ID KV1W_HUMAN
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Best Local 3
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MCKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR, A01936; KWSC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                      QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                         59 QOKPGKAPKLLIYAASSLOSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQOSYSTLI 118
                                                                                                                                                                                                                                                                58
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                               Mús musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_raxID-10090;
                                                                                                                                                                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                 COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                    Length 129;
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FRAMEWORK-4.
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                                                                                              MW; F941FA07D4AFC2F9 CRC64;
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Pred. No. 3.1e-31;
1; Mismatches 12;
                                                                                                                                                    Score 476; DB 1;
Pred. No. 1.8e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CBPC 101.
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79.38; Prec
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73.3%;
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129 AA;
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111 AA;
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QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation. Implications for etiology and immunotherapy.";
J. EXP. Med. 167:840-852(1988).
-!- DISEASE: THE PROFILI IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-71032830; PubMed-4097974;
Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin
                                                                                                                                                                               IG KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                           FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                                                                                                                                                                                    7395528EA2BB74D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Hau.
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                                                                 PIR, PLO021; K3HUHI.
HSSP, P01789; IMCP.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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129
129 AA;
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                                                         LEUKEMIA.
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KV1H_HUMAN
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MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated Kappa 11ght chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic
                                                                                                         1 DIVLIQSPASLAVSLGQRATISCKASQSLDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              MEDELINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 462.5; DB 1; Length 110; 79.3%; Pred. No. 1.7e-30;
 61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCHQS-EDPWTFGSGTKLEIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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38 COMPLEMENTARITY-DETERMINING-
53 FRAMEWORK-2.
60 COMPLEMENTARITY-DETERMINING-
92 FRAMEWORK-3.
110 COMPLEMENTARITY-DETERMINING-
110 FRAMEWORK-4.
92 BY SIMILARITY.
92 BY SIMILARITY.
93 BY SIMILARITY.
94 BY SIMILARITY.
95 BY SIMILARITY.
96 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                  Nature 276:785-790(1978).
PIR: D01937; KTWSI0.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv: 1.
Immunoglobulin V region.
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P18136;
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Matches 8
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                                                                                                                              Gaps
                                                                                                                                                        21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86041854; PubMed-2997713;
Marsh P., Mills F., Gould H.;
Defection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                     Ig kappa chain V-IV region B17 precursor.

Mono saptens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                              4;
                                                                                                                                                                                    81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY-DETERMINING-1.
                    COMPLEMENTARITY - DETERMINING - 2.
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                                     COMPLEMENTARITY - DETERMINING - 3
                                                                                                          Length 108;
                                                                                                       36.9%; Score 457; DB 1; Length 10:
79.5%; Pred. No. 4.7e-30;
.lve 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                            08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                                                                 01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                        134 AA
                                                          BY SIMILARITY.
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                                                FRAMEWORK - 4
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                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A01905; K4HUI7.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
                                                                            11671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X02990; CAA26733.1; -.
                                                                                                                           89; Conservative
                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO 76.
                                                                                                                                                                                                                                                      KV4C_HUMAN
P06314;
                                                                                                                                                                                                                                                                                                                                                                                                     cDNA probe.
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SEQUENCE
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Best Local 9
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-I MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW V-II KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

-I MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR; A01871; KIHULY.

HSSP: P01607; IREI.

InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                             11 KLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWTFGQGTKV 130
                                                                                                                                                                                                                                                                                                     KLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKV 128
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGD--SYMNWYQQKPGQAP 68
                                                                                                                                                                                                                                                    11 LILWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQQKPGQPP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capra J.D., Klapper D.G.;
"Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                           5;
                                                                                                             36.5%; Score 452; DB 1; Length 134; llarity 71.8%; Pred. No. 1.5e-29; Conservative 10; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 449; DB 1; Length 108;
Pred. No. 2e-29;
8; Mismatches 12; Indels
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114 BY SIMILARITY.
134
14966 MW; 6413A22FD0738832 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Lay.
Homo sapiens (Human).
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MEDLINE-77038198; Pubmed-824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV1M_HUMAN STANDARD; F
P01605;
21-JUL-1986 (Rel. 01, Created)
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illarity 78.6%;
Conservative 6
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SMART; SM00406; IGv; i.
Immunoglobulin V region
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Matches 89; Conserv
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Search completed: August 14, 2002, 15:23:13 Job time: 686 sec

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Q96169 homo sapien Q9u183 homo sapien Q91182 m adult mal Q9u186 homo sapien Q9u185 homo sapien

0994f0 mus musculu 091180 mus musculu 0920e6 mus musculu 0920e5 mus musculu 099174 mus musculu 091778 mus musculu 09176 mus musculu 09176 mus musculu 09182 mus musculu 09182 mus musculu 09184 mus musculu 09184 mus musculu 0908551 mus musculu 090859 homo sapien 09680 homo sapien 096844 mus musculu 09086 homo sapien 09684 mus musculu 0908182 homo sapien 09680 homo sapien 09684 mus musculu 0908181 homo sapien 09680 homo sapien 096801 homo sapien 096811 homo sapien 096911 homo sapien 096911 homo sapien 096911 homo sapien 096101 homo sapien 096101 homo sapien

Q90529 ginglymosto Q96jd2 homo sapien Q96jd0 homo sapien

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Thu Aug 15 07:55:57 2002
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Run on:

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 26. 31 KDA PROTEIN.
MUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
TISSUE.;
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illarity 59.0%; Pred. No. 1e-57;
Conservative 39; Mismatches 56; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL.
BOC02035; AAH02035.1; -.
EMBL.
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096169
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Best Local Similarity
Matches 138; Conserv
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    RESULT
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                                                                                                                                                                                                                                                            1 METDTILLEWVLLLEWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein – protein search, using sw model
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Q9R1A5
Q91W12
Q91XL0
Q9UL77
Q96SA9
Q9UL70
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Q920E9
Q9UL78
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Gapop 10.0 , Gapext 0.5
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Q99M11
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Q96PF6
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705.5
705.5
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434.5
434.5
433
430.5
429
429
433
430.5
439
568.5
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                      184
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                                                                                                65 GQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYFFGS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S THE STATE STATES SENT STATES STATES
                                                                                                                                                                      6 ILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDY-DGDSYMNWYQQKP
                                                                                                                                                    125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 739; DB 11; Length 2; Pred. No. 1e-56; 33; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292; AAH15292.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BODOBOE6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL 25.9 KDA PROTEIN.
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60.18;
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Best Local Similarity 60.19
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                Q91WF8;
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                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                      KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ 190
                                                                                                                                                                                                                                                                                                                                                                          81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                             Gaps
                                                                                                                                                                                                              11 LLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKL 70
                                                                                                                                                                                                                                             65
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                        Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                              186 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 233
                                                                                                                                                                             Indels
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                      233 AA; 25781 MW; B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52BA205FDE995E2A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                        59.7%; Score 738; DB 11;
63.2%; Pred. No. 1.2e-56;
ive 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%; Score 721; DB 11; 62.8%; Pred. No. 3.3e-55;
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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23922 MW;
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                                                                                                                                                                             Matches 144; Conservative
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                                                 Hypothetical protein.
NON_TER 1
SEQUENCE 233 AA; 2
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214 AA;
                                                                                                                                        Query Match
Best Local Similarity
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Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Query Match
Best Local Similarity
Matches 133; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 SEQUENCE
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141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAP 137
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STRAIN=C57BL/6J; TISSUE-KIDNEY;
Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   091W12;
01-DEC-2001 (TERBLrel. 19, Created)
01-DEC-2001 (TERBLrel. 19, Last sequence update)
01-DEC-2001 (TERBLrel. 19, Last annotation update)
01-DEC-2001 (TERBLrel. 19, Last annotate)
01-DEC-2001 (TERBLrel. 19, Last sequence)
01-DEC-2001 (TERBLRel. 19, 
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091XL0;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLOME: 06100100P20, FULL INSERT SEQUENCE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006643; AAH06643.1; -. SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                        235 AA
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TISSUE=BREAST TUMOR;
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1091W12
110 D1402
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STRAIN=C57BL/63; TISSUE=KIDNEY;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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prepare full-length cDNA lbraries for rapid discovery of new genes.";
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XX MEDLINE-20530913; PubMed=11076861;
XX MEDLINE-20530913; PubMed=11076861;
XX A Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
XX Sonno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
XX Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
XX Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
XX Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K.,
XX Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
XX Noraaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
XX RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1712(2000).

REMEL: AKO02514: BAB22154.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium.; "Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 2.2e-53;
3; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-KIDNEY;
MEDLINE-99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE-21085660; PubMed-11217851;
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DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polygeactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.1%; Score 459.5; DB 4; Length 107; 83.0%; Pred. No. 8.8e-33; Live 7; Mismatches 7; Indels 5
                                                                                                                                                                                                                                                                                                                                                             Score 467; DB 4; Length 108;
Pred. No. 2e-33;
                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
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108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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EMBL: AF035037; AADS6273.1; -.
HSSP; P01607; IREI.
108 AA
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                       Created)
PRT;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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82.1%;
                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
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Matches 93; Conservative
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PRELIMINARY;
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                                                                                 Homo sapiens (Human)
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                                                                                                                    NCBI_TaxID=9606;
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                     Query Match 36.1%; Score 446; DB 4; Length 108; Best Local Similarity 77.7%; Pred. No. 1.3e-31; Matches 87; Conservative 9; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiéns (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ciin. Immunol, Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR00047; Ig; 1.
NON_TER.
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21361171; PubMed-11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human),
Usukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                           35.1%; Score 434.5; DB 4; Length 107; 77.7%; Pred. No. 1.3e-30; Live 10; Mismatches 10; Indels 5;
                                                                                                                                                                                                    81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                           35.1%; Score 434; DB 4; Length 116; 70.8%; Pred. No. 1.6e-30; tive 14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 116 116 11735 MW; E796FC2217BFCF57 CRC64;
                                                                                                  107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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Last sequence update)
               Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; IRRI.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                   116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood 98:714-720(2001).
EMBL; AF361758; AAK51465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85; Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                         107
                                                                                                                                     1 Similarity
87; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09UL79;
01-MAY-2000 (
01-MAY-2000 (
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NON_TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                       SDNK1.
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                                                                                                                                                                                                                                               RESULT 11
Q96PF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
Q9UL79
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Matches
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                    SEQUENCE FROM N.A.
BEDILINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 433; DB 4; Length 108;
Pred. No. 1.8e-30;
8; Mismatches 14; Indels
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
(FRAGMENT).
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, PO10013, 7FAB.
Interpro; IPR003599; Ig.
Interpro; IPR003599; Ig.
Interpro; IPR003609; Ig.like.
Interpro; IPR0036009; Ig.like.
Interpro; IPR0036009; Ig.like.
Interpro; IPR003609; Ig.like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ll protein.
235 AA; 25403 MW; 39807BFE6782A3FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.4 KDA PROTEIN.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                         Clin, Immunol, Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; IREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.8%; Score 430.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 1.
SMART; SM00410; IG_like; 2.
FROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetial protein.
SEQUENCE 235 AA; 25403 MW; 39807BF]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.0%;
ilarity 76.8%;
Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; 11. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 86; Conserv
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                                                                                                                                 125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                              67 APKLLIYAASNLESGVPSRFSGS--GSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 APKVLIYGNYNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 APKILIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ--QSNEDPRTFGQ 124
                                               7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQ 66
                                                               6 LLLVFLHHLTGSCAQLVLTQ-PSSVSTSLGSTAKLPCKA--STGNIGDSYVNWYQQYMGR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LLITLLAHCTGSWAQSVLAQ-PPSVSGAPGQTVTISCTGS-STNIGAGYAVHWYQQFPGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQ 66
                                                                                                                                                                                                                                           184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                            180 QGVETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 -VETTKPSKQSNNKYAASSYLSLTPPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.7%; Score 429; DB 4; Length 236; 42.4%; Pred. No. 1.1e-29; Ive 39; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12876.1; -.
24712 MW; 7EC9FB3622FED957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:17259).
HOMO saplens (Human).
 Pred. No. 8.3e-30;
; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                          236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AA.
               37; Mismatches
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
 42.68;
Local Similarity 42.6 nes 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.49
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                         Q96E61;
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Best Loca
Matches
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August 14, 2002, 15:15:35; Search time 230.21 Seconds (without alignments) 114.832 Million cell updates/sec
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
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| SIDSI/gcgdata/hold-geneseqy-embl/AA1987.DAT:*
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                                                                                                                                                                                                                                                                                                                     1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1237
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length: 2000000000
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Perfect score:
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Maximum I
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/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1999.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2000.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2001.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

/SIDS1/gogdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*/SIDS1/gogdata/hold-geneseq/geneseqp-embl/AA1992.DAT:\*/SIDS1/gogdata/hold-geneseq/geneseqp-embl/AA1993.DAT:\*

/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

Description	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas
SUMMARIES	AAW90932	AAW90930	AAW90931	AAW83034	AAB14777	AAW90927	AAW83031	AAB14772	AAW90922	AAW83032	AAB14773
DB	21	21	21	19	21	21	19	21	21	19	21
% Query Match Length DB	238	238	238	238	238	238	238	238	238	238	238
% Query Match	100.0	66.66	9.66	94.9	94.9	94.9	94.5	94.5	94.5	93.5	93.5
Score	1237	1236	1232	1174	1174	1174	1169	1169	1169	1156	1156
Result No.	<b>.</b>	7	ო	4	Ŋ	9	7	æ	6	10	11

1156   93.5   238   12   AAM83035   Humanised anti-Fea							
13   1155   93.4   238   19   AAM87035   Anti-Teak humanised anti-1   1155   93.4   238   21   AAM87028   Humanised anti-1   1155   93.4   238   21   AAM87023   Anti-Teak humanised anti-1   1154   93.3   238   21   AAM87023   Anti-Teak humanised anti-1   1154   93.3   238   21   AAM87024   Humanised anti-1   1154   93.3   238   218   21   AAM870250   Light chain and   22   1099   88.8   218   22   AAM87024   Humanised Mazilla   AAM87031   Humanised Mazilla   AAM87031   Humanised Mazilla   AAM87031   Humanised Mazilla   AAM87031   AAM97031   AAM87031   AAM870332   AAM870333   AAM	1	1	93.5	238	21	AAW90923	
14   1155   93.4   238   21   AAB14778   Humanised anti-   1154   93.4   238   12   AAW90928   Humanised anti-   1154   93.3   238   13   AAW90928   Humanised anti-   1154   93.3   238   13   AAW90928   Auti-res humanised anti-   1154   93.3   238   21   AAW90932   Auti-res humanised     155   1076   87.0   218   22   AAW90932   Auti-res humanised     155   1073   86.7   218   22   AAW90932   Autimanised     155   1074   84.3   237   21   AAW90932   Autimanised     155   1075   82.0   233   14   AAR830777   AAW90932   Auti-res humanised     155   1075   82.0   233   14   AAR830777   AAW90932   Autimanised     155	٦	_	93.4	238	19	AAW83035	human
15   1155   93.4   238   21   AAM90928   Humanised Humanised anti-   16   1154   93.3   238   12   AAM909924   Humanised anti-   18   1154   93.3   238   21   AAM909924   Humanised anti-   19   11154   93.3   238   21   AAM909924   Humanised anti-   19   11154   93.3   238   21   AAM909924   Humanised anti-   10   11154   93.3   238   21   AAM909924   Humanised anti-   11154   93.3   238   21   AAM9092565   Humanised anti-   11154   93.3   238   21   AAM90932   Humanised anti-   11154   93.3   238   21   AAM90932     11154   93.3   238   21   AAM90932   Humanised anti-   11154   93.3   218   21   AAM90932   Humanised anti-   11154   93.3   21   AAM90932   Humanised anti-   11154   1021   B2.5   AAM57614   Humanised 501.1     11154   AAM90932   Humanised 501.1     11154   Humanised 501.1     11154   Humanised 501.1     11155   Humanised	_		93.4	238	21	AAB14778	anti
16   1154   93.3   238   19   AAW93033   Anti-Fas humanised anti-16   1154   93.3   238   21   AAW90924   Humanised anti-19   1113   90.0   218   18   AAW35658   Humanised anti-20   1099   80.8   218   21   AAW95659   Humanised anti-21   1099   80.8   218   22   AAW95658   Humanised anti-21   1099   80.8   218   22   AAW95650   Humanised Anti-19   1009   80.8   218   22   AAW95660   Humanised MaEll 22   AAW95660   Humanised MaEll 23   1009   80.8   218   20   AAW95660   Humanised MaEll 24   AAR95660   Mus musculus an macculus and maccul	-	П	e.	238	21	AAW90928	Humanised HFE7A de
17   1154   93.3   238   21   AAB14774   Humanised antti-   1154   93.3   238   21   AAB14774   Humanised antti-   19   1113   90.0   218   18   AAW13563   Humanised antti-   20   1099   88.8   218   21   AAW19558   Humanised antti-   21   1099   88.8   218   21   AAW19558   Humanised antti-   22   1099   88.8   218   21   AAW195697   Humanised antti-   23   1095   88.8   218   21   AAW19597   Humanised antti-   24   1076   87.0   218   20   AAW19560   Mus musculus an   25   1076   87.0   218   20   AAW19560   Mus musculus an   26   1076   87.0   218   20   AAW19560   Mus musculus an   27   1076   87.0   218   20   AAW19560   Mus musculus an   28   1073   86.7   218   20   AAW19560   Mus musculus an   31   1073   86.7   218   20   AAW19560   Mus musculus an   32   1073   86.7   218   22   AAB7691   Mus musculus an   33   1073   86.7   218   22   AAB7691   Mus musculus an   34   1073   86.7   218   22   AAB7691   Mus musculus an   35   1073   86.7   218   22   AAB7691   Mus musculus an   36   1073   86.7   218   22   AAB7691   Human ingrAm-1 is   36   1073   86.7   218   22   AAB7692   Human ingrAm-1 is   37   1044.5   84.8   237   21   AAY6628   Human ingrAm-1 is   38   1046.5   84.6   237   21   AAY6628   Human ingrAm-1 is   38   1046.5   84.1   237   21   AAY6628   Human ingrAm-1 is   41   1040   84.1   237   21   AAY6628   Human ingrAm-1 is   42   1021   82.6   233   14   AAR30777   AAR90932;    AAW90932   AAW90932;   AAW90932;   AAW90932;	1	-	ε,	238	19	AAW83033	Anti-Fas humanised
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Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antininfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; odogasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Humanised anti-Fas designed light chain Leu 3 protein.

98JP-0276881. 98JP-0276882. 99EP-0307711. 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; EP990663-A2 05-APR-2000 Synthetic. 

(SANY ) SANKYO CO LTD.

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This invention describes a nover numanized anti-res annibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidabetic, anti-allergic, anti-arthritic, antidiabetic, anti-antimiterial immunosuppressive, thyromimetic, antitarteriosclerotic, cardiant and hepatropic activity. (I) induce antitrheumatic, nephrotropic, antinifertility, thyromimetic, antitarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent classase associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic disease, solorederma, Goodpasture syndrome, Crohn's fully nost disease, Slorgen's syndrome, pernicicus or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral CC andiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral CC Inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents when the active is sequence represents.
                                                                                                                                                                   New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                               This invention describes a novel humanized anti-Fas antibody-like
                           Takahashi T;
                        Tamaki I,
                           Nakahara K,
                                                                                                                                                                                                                                                                                     Claim 3; Page 161-162; 263pp; English.
                           Haruyama H,
                                                                              WPI; 2000-258930/23.
                                                                                                               N-PSDB; AAA11633
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¥ 238 Sequence

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                                                                                                                              121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                               Gaps
                                                                       181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                           1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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  Length 238;
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  DB 21;
100.0%; Score 1237; DB 21
100.0%; Pred. No. 4.3e-62;
ive 0; Mismatches 0;
Query Match 100.
Best Local Similarity 100.
Matches 238; Conservative
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Humanised anti-Fas designed light chain Leu 1 protein. AAW90930 standard; Protein; 238 AA. 08-AUG-2000 (first entry) AAW90930; AAW90930

anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; antir-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease, rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia, Addison's disease; scleroderma; sterility; odopasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

EP990663-A2

Synthetic.

05-APR-2000.

99EP-0307711. 29-SEP-1999;

98JP-0276882. 98JP-0276881 30-SEP-1998; 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Haruyama H, Nakahara K, Tamaki I, Takahashi T; Serizawa N,

WPI; 2000-258930/23. N-PSDB; AAA11631 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 3; Page 156-157; 263pp; English.

This invention describes a novel numarized anti-ras antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

capptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

anti-anemic, antidiabetic, anti-alterpic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

capping in this information of ligand binding. (I) are used to treat and/or prevent

clisanses associated with the Fas/Fas ligand system, especially systemic

diseases associated with the Fas/Fas ligand system, especially graft

coversus host disease, Sjorgen's syndrome, pernicidous or hypoplastic

coversus host disease, sjorgen's syndrome, pernicidous or hypoplastic

anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

disease, autolmmune hemolytic anemia, sterility, myasthenia gravis,

multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosolerosis, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

(B, C or D) or alcoholic, and transplant rejection. (I) selectively

chihibit apoptosis in normal cells but selectively induce it in abnormal

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

chouse inducing a human anti-murine antibody response. This sequence represents

c humanised anti-Fas antibody light ch This invention describes a novel humanized anti-Fas antibody-like 

238 AA; Seguence

Gaps ; Length 238; Indels Score 1236; DB 21; Pred. No. 4.9e-62; 1; Mismatches 0; 99.68; 99.68; Query Match 99.99
Best Local Similarity 99.69
Matches 237; Conservative

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1 METDTILLWYLLLWYPGSTGDIVLTQSPSSLSASVGDRYTITCKASQSVDYDGDSYMNWY 60

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple scleroderms; crohn's disease; sterility; myasthenia gravis; multiple sclerodsis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosmodulatory, dermatological, immunosuppressive, thyromimetic, antinfertility, neuroprotective, antiarteriosclerctic, antinfertility, neuroprotective, antiarteriosclerctic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                         QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                          121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                   GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised anti-Fas designed light chain Leu 2 protein.
                                                                                                                                                                                                                                                                                                                                            AAW90931 standard; Protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-258930/23.
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                                                                                                                                                                                                                                                                                                                                                                                 AAW90931;
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                                                                                                                             disease, autoimmune hemolytic anemals, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B; C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine fiss, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody light chain construct designated Leu 2 which is described in the method of the invention.
diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematcosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndreme, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1232; DB 21; Length 238; Pred. No. 8.1e-62;
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glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
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thrombopenia purpura; insulin-dependent diabetes; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-Fas humanised antibody HFE7A light chain PDHH type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.2%; Score ... 99.2%; Pred. No. 8.1e-v
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21..238
/label= Mat_protein
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/label= Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
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61 QOKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120 

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1 metdtillwvlllwvpgstgeivltgspgtlslspgeratlsckasgsvdydgdsymnwy 60

121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

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chain of murine and sequence of the Pinn Lype Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49K, H80S, P81R, V82L, E84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coll pHSHH5 SANK 7039B harbors plasmid pHSHH5 carrying a fusion fragment of the humanised PDHH type HFF7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is methods for producing humanised antibodies by culturing host cells. Humanised versions of HFF7A (see AAW83031-37), like native HFF7A, are capable of inducing apoptosis in abnormal cells. Cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, carefurents of disease, Sjogren syndrome, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, disease, rheumatoid arthritis, autoimmune haemolytic anaemia, eterility manaemia, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the PDHH type humanised light
                                                                                                                                                                                                                                                                                                                                                                        In O, Kimihisa I;
Tohru T;
                                                                                                                                                                                                                                                                                                                                                                          Jun 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 218; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Hideyuki H, Hiroko Y, J
O, Nobufusa S, Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases e.g. autoimmune disease, myocarditis, hepatitis and AIDS
                                                                        74..80
/label- CDR_L2
/note- "claim 9"
                'label" Constant
                                                           /note= "claim 9"
                                                                                                                                                      'note= "claim 9"
                              44..58
/label= CDR_L1
                                                                                                                                         CDR_L3
                                                                                                                                                                                                                                                                          97JP-0276064.
97JP-0082953.
97JP-0169088.
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                                                                                                                       113..121
/label- C
                                                                                                                                                                                                                                                                                                                                                                                        Masahiko O, Nobufusa
                                                                                                                                                                                                                                                                                                                                          SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-543440/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AA;
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01-APR-1997;
25-JUN-1997;
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sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
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METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                   Indels
Pred. No. 1.4e-58;
9; Mismatches 7;
Local Similarity 93.3 es 222; Conservative
   Best Loca
Matches
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94.9%; Score 1174; DB 19; Length 238; 93.3%; Pred. No. 1.4e-58;

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFF7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis. AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                           Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                      Humanised anti-Fas antibody light chain, SEQ ID NO:107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 101; 139pp; Japanese.
                                                                                                                                       AAB14777 standard; Protein; 238 AA
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                                                                                                                                                                                                                   24-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-arlbritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatold arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; anemia; Addison's disease; scleroderma; sterility; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                              QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                           TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                              Gaps
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                                 Indels
Pred. No. 1.4e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised HFE7A designed light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 141-142; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                    AAW90927 standard; Protein; 238 AA.
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             93.3%;
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98JP-0276882.
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               Similarity 93.3
22; Conservative
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                              Matches
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus errythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernficious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, starility, myasthenia gravis,
anultiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholie), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1174; DB 21; Length 238;
Pred. No. 1.4e-58;
9; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-Fas humanised antibody HFE7A light chain HH type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atopy; arteriosclerosis; myocarditis; cardiomyopathy;
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93.38;
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/label= Sig\_peptide

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This is the amino acid sequence of the HH type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM8014) entailed making P47A, K49R, H80S, P81R, W81E. E84A. E85A. A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (see AAM8014) entailed making a lubstitutions; these residues are conserved in the human light sharpers plasmid pHSGHH7 carrying a fusion fragment of the humanised HH type HFE7A light chain and DNA encoding the region of human mumunoglobulin kappa chain, and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A apoptosis in abnormal cells expressing Fas, and of inhibiting pappitosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas lighand interactions, and also to treat such diseases including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, scleroderma, Goodpasture syndrome, Crohn's disease, thermatoid arthitis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura gravis, multiple sclerosis, Basedow's disease, thrombopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 199-199; 292pp; English.
21..238
/label= Mat_protein
                                                      /label- Variable
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/label= Constant
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/label- CDR_L3
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/label= CDR_L1
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97JP-0169088
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, alongy, arteriosclerosis, myocarditis, cardiomyopathy, and organ graft rejection. Sequences AABI4772-B14774 and AABI4777-B14778 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy, arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                               QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                   TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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               METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatitis; AIDS; graft rejection; light chain.
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Chimeric - Homo sapiens.
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238 AA;

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Gaps

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Score 1169; DB 19; Length 238; Pred. No. 2.7e-58; 9; Mismatches 8; Indels 0;

6

Conservative

Best Local Similarity Matches 221; Conserv

Query Match

94.5%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized anti-Fas antibody, useful for treating or preventing e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                             QOKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                   Gaps
                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                         181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                          Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory or autoimmune disease, induces apoptosis selectively cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-Fas antibody HFE7A light chain HH type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi T;
 Length 238;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example reference 14; Page 114-115; 263pp; English.
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   DB 21;
 Score 1169; DB 21
Pred. No. 2.7e-58;
                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      AAW90922 standard; Protein; 238 AA
94.5%;
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                                221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANY ) SANKYO CO LID.
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               Similarity
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 Query Match
                  Best Local
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cc Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, immunodulatory, dermatological, immunosuppressive, thyromimetic, antirinal immunosuppressive, thyromimetic, antirinal immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, cantirheumatic, nephrotropic, antiinfertility, neuroprotective, antiinfertility, neuroprotective, antiinfertility, neuroprotective, cantirheumatic, nephrotropic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic upous erythematosus, Hashimoto disease, rheumatoid arthritis, graft oversus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, cleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, Sterility, myasthenia gravis, antiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepaticis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minc mutive disease models. (I) act on the active site of Fas, i.e. they minc mutive disease models. (I) act on the active site of Fas, i.e. they minc inducing a human anti-murine antibody HEFAA light chain H type which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis; HEFA, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; sjotemic lupus erythematosus; graft versus host disease; sjotem syndrome; pernicious anaemia; Addison's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.5%; Score 1169; DB 21; Length 238; 92.9%; Pred. No. 2.7e-58; ive 9; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-Fas humanised antibody HFE7A light chain HM type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AA;
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Homo sapiens. Synthetic.

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This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entailed making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coll pHSGHM1 SANK 73597 harbors plasmid pHSGHM7 carrying a fusion fragment of the humanised HM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells. Cells. The humanised antibodies are used to evaluate, in animal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve FrasFras ligand interactions, and also to treat such diseases, including autoimmune disease, stearchards and shows a syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Croh's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, eteriity mitting multiple collons disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, attopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jun O, Kimihisa I;
Location/Qualifiers
                               'label Sig_peptide
                                             21..238
/label= Mat_protein
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                                                                                                                                                                                          74..80
/label- CDR_L2
/note= "claim 9"
                                                                              21..131
/label= Variable
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/note= "claim 9"
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Masahiko O, Nobufusa S, Shin Y
                                                                                                                                             44..58
/label= CDR_L1
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25-JUN-1997;
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 Key
Peptide
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas Ilgand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFF7A, or a humanised version of HFF7A containing identical CDRs (complementarity determining regions) to antibody HFF7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                        61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                              121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                        Gaps
                                                                               1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                           181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Length 238;
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                                           Indels
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 93.5%; Score 1156; DB 19; 92.0%; Pred. No. 1.4e-57;
                                         6
                                         10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB14773 standard; Protein; 238 AA.
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                                       Matches 219; Conservative
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Chimeric - Homo sapiens.
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N-PSDB; AAA72125.
                       Best Local Similarity
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     Query Match
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                                                                                                                                                                                                     121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                               QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSNEDPR 120
                                                                                                     Gaps
                                                                                                                                              1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                        238
                                                                                                                                                                                                                                                                                                                   antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                                                                                                                                                                                                                                                                                      GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                     Length 238;
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                                                                                                    Indels
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                                                                     Score llos; ______
Pred. No. 1.4e-57;
                                                                     93.5%; Score 1156; 92.0%; Pred. No. 1.4
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98JP-0276882,
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                                                                                                  Conservative
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                                                                                  Similarity
                            238 AA;
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30-SEP-1998;
                                                                                      Best Local Simi
Matches 219;
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                            Sequence
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disease, autoimmune hemolytic annual, solutions of gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand do not induce liver disease, and have reduced risk of inducing a human santi-murine antibody response. This sequence represents a humanised anti-Fas antibody response. This sequence represents the method described in the invention.
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                 immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
acpy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibody; mouse; Fas; humanised antibody
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92.0%;
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Gaps

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Indels

Length 238;

DB 19; . 6

93.4%; Score 1155; DB 19 92.0%; Pred. No. 1.6e-57; 10; Mismatches

Conservative

Matches 219;

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Query Match Best Local Similarity

238 AA;

Sequence

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61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120 

1 METDTILLEWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60 

121 TFGOGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

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181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

AAB14778 standard; Protein; 238 AA.

AAB14778

(first entry)

24 - NOV - 2000

AAB14778;

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chain of murine anti-human Pass monoclonal antibody HFEFA.

Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell Escherichia coli pHSHM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFEFA light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERN BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFEFA (see AAW83031-37), like native HFEFA, are capable of inducting apoptosis in abnormal cells. Crist of inducting apoptosis in abnormal cells. The humanised antibodies are used to evaluate, in animal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, carafteriate syndrome, pernicious anamia, and slease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid artaritis, autoimmune haemolytic anaemia, sterility. Myasthonia gravit militins autoimmune haemolytic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Page 220-221; 292pp; English.
                                                                  ...20
|abel= Sig_peptide
|1..238
                                               Location/Qualifiers
                                                                                                              /label= Mat_protein
                                                                                                                           21..131
/label= Variable
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                                                                                                                                                                                                                           'note= "claim 9"
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                                                                                                                                                                                                                                                                                                    /label= CDR_L3
/note= "claim 9"
                                                                                                                                                                                                                                       74..80
/label= CDR_L2
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/label= CDR_L1
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97JP-0082953.
97JP-0169088.
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Homo sapiens.
Synthetic.
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25-JUN-1997;
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                                                              Peptide
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or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autolmmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
                                                                                                                                                                                                                                                                                                                   murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                        Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                  Humanised anti-Fas antibody light chain, SEQ ID NO:109.
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Chimeric - Homo sapiens.
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glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
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                                                                                                                   Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised HFE7A designed light chain protein #2.
                                                                                                                   93.4%; Score 1155; DB 2.92.0%; Pred. No. 1.6e-57
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This invention describes a novel numenized anti-ras antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas igand system, by binding to Fas on the cell surface, and prevents capperosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antaclogical, immunosuppressive, thyromimetic, antidiabetic, antidiateriosclerotic, cardiant and hepatropic activity. (1) induce antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive cinhibition of ligand binding. (1) are used to treat and/or prevent disease associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Cro anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral cells or alcoholic), and transplant rejection. (1) selectively cinhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-marine antibody response. This sequence represents con human anti-marine antibody response. This sequence represents a humanised anti-marine antibody response. This sequence represents con human anti-marine antibody response. This sequence represents a humanised anti-marine antibody response. This sequence represents and murine the active site of Fas, i.e. they minic the human anti-marine antibody response. The net
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                                                                                                                                                  This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Example reference 21; Page 144-145; 263pp; English.
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; Pred. No. 1.6e-57;
10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the method described in the invention
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Best Local Similarity 92.0
Matches 219; Conservative
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Sequence Sequence Sequence

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Sequence 2, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TTLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 218;
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Pred. No. 5.3e-88;
                      US-08 437-642B-40

US-09-097-309-2

US-09-097-309-2

US-09-097-309-6

US-09-097-309-6

US-09-097-309-6

US-09-097-309-6

US-09-027-356-2

US-09-027-449-62

US-09-026-985-62

US-09-026-985-62

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-72

US-09-026-985-72

US-09-026-985-72
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 89:
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 96:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%;
98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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STREET: 805 Thii
CITY: New York
STATE: New YOrk
COUNTRY: U.S.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-13152-2
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LENGTH:
     (without alignments)
70.141 Million cell updates/sec
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                                                                                                                                                                                  August 14, 2002, 15:17:03; Search time 82.88 Seconds
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-296-005-17

US-09-296-005-18

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US-08-437-642B-39
PCT-US93-07832-39
US-07-934-373C-40
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US-08-887-352B-13
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1237
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length: 2000000000
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Sequence No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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   2; Indels
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Pred. No. 8.3e-87;
3; Mismatches 3;
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   Mismatches
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Best Local Similarity 97.2%;
Matches 212; Conservative
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Amino Acid
   Conservative
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201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     Sequence 9, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/466,151
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/406163
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 0/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/7879495
FILING DATE: 0/-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/74768
FILING DATE: 14-ANG-1991
ATTORNEY/GENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1489
TELEFAX: 650/952-9881
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                            Genentech, Inc.
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CITY: South San Francisco
STATE: California
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Amino Acid
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81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                      Length 218;
   ; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
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                                                                                      Score 1099; DB 4; Length 2
Pred. No. 8.3e-87;
3; Mismatches 3; Indels
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/485,899
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 9, Application US/08466163B
; Patent No. 6329509
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                                                                                      Query Match 88.8%;
Best Local Similarity 97.2%;
Matches 212; Conservative
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SEQ ID NO 9
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                                                                                                                               Sequence 13, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT FPLING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
LENGTH: 218
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GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.8%; Score 1099; DB 4; Length 218; Best Local Similarity 97.2%; Pred. No. 8.3e-87; Matches 212; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-109-207C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                      STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Artificial LOCATION: 1-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 218
TYPE: PRT
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                                                                                                      181
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                       81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                           81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYMNWYQQKPGKAPKLLIYAASYLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIVLIQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1073; DB 2;
Pred. No. 1.4e-84;
6; Mismatches 5;
                                                                                                                                                                                         STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: 3.5 inch, 1.44 Mb floppy disk IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/887,352B
03-Jul-1997
                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08887352B Patent No. 5994511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
MAME: SYODOGA, CTRAGG G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PI.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.7%;
Best Local Similarity 95.0%;
Matches 207; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
SOFTWARE: WinPatin (Gene
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 03-Jul-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPCKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 7.7e-85;
5; Mismatches 5; Indels
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87.0%; Score 1076; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 7.7e-85;
Matches 208; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1-218
. OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: E27 anti-IgE antibody light chain US-09-054-255-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                      Sequence 1, Application US/09282505A
Patent No. 6194551
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: Pl266R1
CURRENT APPLICATION UNDBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ESONE EXINAGUESE IGUSOGIE et al.
TITLE OF INVENTION: POLYPEPTIGE VARIANTS
FILE REFERENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09054255 Patent No. 6242195
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 87.0%;
Local Similarity 95.4%;
hes 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                           RESULT 7
US-09-282-505-1
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US-09-054-255-1
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Query Match

Matches

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SEQ ID NO 1

FEATURE:

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Gaps

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FEATURE:

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 24, Application US/08887352B; Patent No. 5994511 GENERAL INPORMATION: GENERAL APPLICANT: Henry B. Lowman, Leonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/925-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%;
95.0%;
                                  : 1 DNA Way
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
    CORRESPONDENCE ADDRESS
                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linear
                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-887-352B-19
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                                                                            STATE: C
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                                                                                         Sequence 17, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY, AGENT INPORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1073; DB 2;
Pred. No. 1.4e-84;
6; Mismatches 5;
181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207; Conservative
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APPLICANT: Henry B.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 207; Conserva
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                                                                                                                                                                                                                                                                                                                                             94080
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US-08-887-352B-19
                                                        RESULT 10
US-08-887-352B-17
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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                                                                                                                                                                             141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                 Gaps
                                                                                        21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                ö
    Length 218;
Score 1073; DB 2;
Pred. No. 1.4e-84;
6; Mismatches 5;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept,
FILE REPERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILEM DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09109207C
Patent NO. 617213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula Method of Improving Polypep
FILE REFERENCE: P1123R1
CURRENT PELLING DATE: 1998-06-30
PRIOR PAPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
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            IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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95.0%; Pred. No. 1.4e-84;
tive 6; Mismatches 5;
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                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09109207C Patent No. 6172213
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Best Local Similarity 95.0
Matches 207; Conservative
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US-09-109-207C-17
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LENGTH: 218
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 15
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Pred. No. 1.4e-84;
6; Mismatches 5;
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95.0%; Pred. No. 1.4e-84;
live 6; Mismatches 5;
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03-Jul-1997
11: 530
                       APPLICATION NUMBER: US/08/887,3521
CLASSIFICATION: U3-1-1997
CLASSIFICATION: 03-510
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 90.044
REFERENCE/DOCKET NUMBER: P1123
TELEPHONE: 650/25-1489
TELEPHONE: 650/25-1489
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09109207C Patent No. 6172213 GENERAL INFORMATION:
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95.0%;
                                                                                                                                                                                                                                                                        LENGTH: 218 amino acids TYPE: Amino Acid
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Best Local Similarity 95.04
Matches 207; Conservative
              CURRENT APPLICATION DATA:
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US-08-887-3528-24
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Best Local Similarity
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) ORGANISM: Artificial
FEATURE:
) NAME/RET: Artificial
| LOCATION: 1-218
| OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19
                                                                                                                ö
                                                                                        Length 218;
                                                                                        Query Match 86.7%; Score 1073; DB 4; Length 2 Best Local Similarity 95.0%; Pred. No. 1.4e-84; Matches 207; Conservative 6; Mismatches 5; Indels
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Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
R;Species: Homo sapiens (man)
R;Specie
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Ig kappa chain pre- Ig kappa chain - h Ig kappa chain - h Ig kappa chain v-J Ig kappa chain pre- Ig light chain - r Ig kappa chain c r Ig kappa chain C r Ig kappa chain C r Ig kappa chain - h	ALIGNMENTS	hain NIG26 precursor - human  Homo sapiens (man)  Homology  Homeki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinod-  to JIPID, November 1998  Homoser: JE0241  Homology immunoglobulin homology  Homology immunoglobulin v region; immunoglobulin homology  Homology immunoglobulin homology immunoglobulin homology  tch  Tobec 198; Score 946.5; DB 2; Length 215;  al Similarity 83.98; Pred. No. 8.7e-55;  BIVITQSPSILSASASVGDRYTITCKASQSVDYDGDSYMNWYQOKPGRAPKLLIYAASNLES 80  HIIII	GIPDRESGESGTDETLITISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEIKRTVAPSVF 117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200 IFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177 IFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 
PLO106 KVMSM6 SA0331 SA0367 KVMS32 SA0367 AA9134 AA9134 AA9134 AA9134 S26653 S26653 S26653 S26631 S26631 S26633 S2663 S266	ALIG	human ision 05 ', M.S.; ship of egion; i mology < Score 9 Pred. N KASQSVDY :	PEDFAVY: YPREAKV(	GLSSPVT)
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144 131 127 127 127 137 145 145 145 1145 1131 1311 1311		hain NIG26 precursor - human Homo sapiens (man)	TASVVCLI TASVVCLI	HKVYACE         KVYACE
44444444444444444444444444444444444444		SULT 1  kappa chain NIG26 pr. Species: Homo saplens Date: 05-Dec-1998 #se Alim, M.A.; Yamaki, S bmitted to JIPID, Now Description: Structury Reference number: JE024 Accession: JE0242 Accession	FSGSGSG DEQLKSG	SKADYEK 
548 531 521 520 520 520 517 517 500 503 503 503 503 503 503 503 503 503		a chain N es: Homo of5-Dec-1 sion: JEO M.A.; Ya ed to JIP ed to JIP iption: S sion: JEO ule type: ues: 1-21 family: i fomily: i fomily: i Local Sim es 183; 21 DIVLTQ 1 EIVLTQ 1 EIVLTQ	G IF	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		RESULT 1 JED242  Ig kappa chain NIC26 precursor - human c; Species: Homo sapiens (man) C; Date: 05-Dec-1998 #sequence_revision C; Accession: JED242  R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Submitted to JIPID, November 1998 A; Description: Structure relationship of A; Reference number: JED241 A; Rolecule type: protein A; Residues: 1-215 < ALIN C; Superfamily: immunoglobulin v region; F; 16-91/Domain: immunoglobulin homology Query Match Best Local Similarity 83.9%; Pred. Matches 183; Conservative 14; Mish Mish Mish Mish Mish Mish Mish Mish	Db 58 Qy 147 Db 118	Oy 201 Db 178

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215;

Length Indels

5;

homology

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C; Accession: JE0241
R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda B; Dimbitched to JIPID, November 1998
A; Description: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: JE0241
A; Reference number: JE0241
A; Accession: JE0241
A; Accession: JE0241
A; Residues: 1-216 < ALI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
E; 16-92/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb.1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GIPDRESGSGSGIDFILITISRLEPEDFAVYXGQQYGSSPLTFGGGTKVEIKRIVAAPSVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 IFPFSDEQLKSGTASYVCLLNNFYPREAKVQWKVDNALQSGNSQESYTEQDSKDSTYSLS 178
                                                                                                                                                                                                                                                                   1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ-PKLLIW-ANVRES
                                                                                                                                                                                                                                                                                                                             81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF
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                    A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.8%; Score 876; DB 2; Best Local Similarity 79.4%; Pred. No. 3.3e-50; Matches 173; Conservative 16; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
                                                                                                                                                              71.7%; Score 886.5; DB 2 ilarity 82.0%; Pred. No. 6.9e-51; Conservative 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 STLTLSKADYEKHKVYAGEVTHOGLSSPVTKSFNRGE 214
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Best Local Similarity
Matches 178; Conserv
    A;Status: preliminary
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C;Species: Homo sapiens (man)
C;Species: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession, A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl A;Reference number: A23746; MUID:91131575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                  GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSNE-DPRTFGQGTKVEIKRTVAAPSV 139
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                                                                                                                                          21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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                                                            Length 215;
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A, Molecule type: protein
A, Residues: 1-215 <ALI>
C, Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                    Indels
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                                                                  .,5e-53;
___18;
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81.3%; Pred. No. 6.3e-52;
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83.6%; Pred. No. 1...
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R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda,
submitted to JIPID, November 1998
F;16-90/Domain: immunoglobulin homology <IMM>
                                                        Query Match
Best Local Similarity 83.6'
Matches 183; Conservative
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Length 216;

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If Xappa chain V region (Mabl3-1) - mouse (fragment)
Nyllernate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68244
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, submitted to the BMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porpha, A;Reference number: S68241
A;Accession: S68241
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A;Residues: 1-218 <TAK>
A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
A;Cross-references: EMBL:D29670; N: Harada, A.; Yamaquchi, H.; Kamachi, M.; Imanaka
FPBS Lett. 375, 273-276, 1995
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C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C; Accession: 3316
A; Description: Isolation and characterisation of sheep kappa light chain cDNA.
A; Reference number: 533161
A; Accession: S33161
A; Status: preliminary
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NGVLNSWIDQDSKDSTYSMSSTLTLTKTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
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Pred. No. 6.9e-42;
y, Mismatches 47; Indels
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A;Nolecule type: mRNA
A;Residues: 'NI',3-212 <TAM>
A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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63.8%;
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Best Local Similarity 63.8%
Matches 139; Conservative
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A; Residues: 1-230 <FOL>
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          R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain A;Reference number: S06084; MUID:90016888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 PRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 WYQQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNED 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METDIILLWYLLLWYPGSTGDIYLTQSPSSLSASYGDRYTITCKASQSYDYDGD--SYMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623; Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623; Storost Email: immunoglobulin v region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin ; Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                               PID:956458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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Pred. No. 2.6e-42;
5; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 240;
                                                                                                                                                                A; Accession: S06084
A; Molecule type: mRNA
A; Rocession: S06084
A; Molecule type: mRNA
A; Cross-references: EMBL: X16129; NID: 956457; PIDN: CAA34256.1; PI
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
E; 1-240/Product: signal sequence #status predicted <NIS>
E; 21-240/Product: ig kappa chain #status predicted <NAT>
E; 153-222/Domain: immunoglobulin homology <NAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.3%; Score 808; DB 2; Length 24 64.2%; Pred. No. 9.7e-46; Live 32; Mismatches 52; Indels
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60.1%;
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Best Local Similarity 60.1<sup>3</sup>
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.3°
Best Local Similarity 64.2°
Matches 154, Conservative
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A, Cross-references: EMBL: C, Superfamily: immunoglob C, Keywords: heteroterrame F; 36-110/Domain: immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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Length 230;

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Length 234;

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WYQQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNED 118
                                                                                                                                                                                                                                                                                                                                                                                    RQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                        1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMN--
                                                                                                                                                                                                                                             PRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                            OSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                     F:1-20/Domain: signal sequence #status predicted <SIG>F:21-234/Product: Ig kappa chain #status predicted <WAT>F:36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                58.9%; Score 728; DB 2; L 57.9%; Pred. No. 1.5e-40; ive 38; Mismatches 55;
                                                                                                                                                                                    Conservative
                                                                                                                                                                 Best Local Similarity
Matches 139; Conserv
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Itle: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr A;Reference number: JC5810; MUID:98063277
A;Accession: JC5810
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C; Accession: 501320
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A; Reference number: 501320; MUID:88329081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is directed against a
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                                                                                                                           66 KAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQG 125
                                                                                                                                                IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                     126 TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
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                      Gaps
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                                                                          DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-234 <DE1>
A;Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLWVLLLW-VPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPG
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0
                                                                                                                                                                                                                                                                            SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                           monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: This catalytic antibody has peroxidase oxidase. It is C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-94/Domain: immunoglobulin homology <IMM>
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
7.9e-42;
ches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.3%; Score 746; DB 2;
64.2%; Pred. No. 9.3e-42;
ive 30; Mismatches 48
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                    Mismatches
   Š.
 Pred.
                 37;
61.8%;
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                   144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-218 <AKA>
Best Local Similarity
Matches 144; Conserv
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Best Local S:
Matches 140;
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Ighthappa chain V region (17/9) - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Al-Mar-1990 #text_change 21-Jan-2000
C; Accession: A31790
R; Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
Biol. Chem. 263, 17100-17105, 1988
A; Title: Preliminary crystallographic data, primary sequence, and binding data for an A; Reference number: A92686; MuID:89034213
A; Accession: A31790
A; Accession: A31790
A; Accession: A31790
A; Residues: 1-220 <SCH>
A; Cross references: GB:M3566; GB:U04061; NID:9533234; PIDN:AAA39162.1; PID:9533235
C; Superfamily: immunoglobulin munoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
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    mouse (fragment)

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Matches 135; Conservative
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Search completed: August 14, 2002, 15:18:59
Job time: 687 sec
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Best Local Simi
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          C. Accession: A56169
R. Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
R. Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
B. Biol. Chem. 270, 6628-6638, 1995
A. Title: Recombinant antibodies in bloactive peptide design.
A; Reference number: A56169, MUID:95204454
A; Accession: A56169
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-210 < MON>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change ll-Jan-2000
C; Accession: S37484
R; Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A; Reference number: S37483
A; Accession: S37484
A; Accession: S37484
A; Accession: S37484
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1.225 < DUC>
A; Cross-references: EMBL:X70424; NID:9406254; PIDN:CAA49869.1; PID:9406255
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
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STLTLTKDEYERHNSYTCEATHKTSTSPI 209
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C;Species: Mus musculus (house mo
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135; Conserv
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Best Local S
Matches 135
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Species: Mus musculus (Nouse mouse)

C; Species: Mus musculus (Nouse mouse)

C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C; Accession: Pc4203

A; Title: Cloning and characterization of cDNAs coding for heavy and light chains of a A; Title: Cloning and characterization of cDNAs coding for heavy and light chains of a A; Reference number: Pc4202; MUID:97082978

A; Reference number: Pc4203

A; Accession: Pc4203

A; Accession: Pc4203

A; Accession: Pc4203

A; Residues: 1-219

C; Comment: This protein is specific for human plasma apolipoprotein A-I of high-demsing C; Superfamily: immunoglobulin V region; immunoglobulin homology

F; 1-112/Domain: V region #status predicted <RG>
F; 113-219/Domain: C region #status predicted <CRG>
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Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
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August 14, 2002, 15:23:13; Search time 53.64 Seconds (without alignments) 171.798 Million cell updates/sec
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1 METDTILLWVLLLWVPGSTG......BVTHQGLSSPVTKSFNRGEC 238
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	P01834 homo sapien	mus n	P01658 mus musculu	P01665 mus musculu	P01666 mus musculu	mus m	homo	P04431 homo sapien	mus m		P01600 homo sapien	mus m	homod	homo	homo	homo	homo	уошо	homo	homo	homo	homo	homo	homo	mus m	homo	homo	homo	homo	homo	homo	P01611 homo sapien	P04432 homo sapien
SUMMAKIES		ID	KAC_HUMAN	KV3I_MOUSE	KV3F_MOUSE	KV3M_MOUSE	KV3N_MOUSE	KV30_MOUSE	KV3L_HUMAN	KV1W_HUMAN	KV3Q_MOUSE	KV3L_MOUSE	KV1H_HUMAN	KV3P_MOUSE	KV3M_HUMAN	KV1G_HUMAN	KV1M_HUMAN	KV1K_HUMAN	KV4C_HUMAN	KV1B_HUMAN	KV1E_HUMAN	KV1F_HUMAN	KV1N_HUMAN	KV1V_HUMAN	KV1A_HUMAN	KV1J_HUMAN	KV3H_MOUSE	KV10_HUMAN	KV1P_HUMAN	KV3H_HUMAN	KV4B_HUMAN	KV1Y_HUMAN	KV1R_HUMAN	KV1S_HUMAN	KV1X_HUMAN
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SE	MENTS	PRT; 106 AA. ed) sequence update) annotation update)	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	[1] SEQUENCE (MYELOMA PROTEIN EU). SEQUENCE (MYELOM4023; PubMed=5489770; Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The covalent Structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."; Biochemistry 9:3155-3161(1970).	gamma G-immunoglobulin. X.	SEQUENCE (BENCE-JONES PROTEIN TI).  SEQUENCE (BENCE-JONES PROTEIN TI).  Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  Suter L., antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";  Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).	14) MEDLINE-81042304; PubMed=6775818; MEDLINE-81042304; PubMed=6775818; Hieter P.A., Max E.E., Seldman J.G., Maizel J.V. Jr., Leder P.; "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";	Hess M., Langer B., Ponstingl H., Watanabe S.; '); function, pp.57-74, Academic Press, CUM). 23;
KV3J_MOUSE KV3K_HUMAN KV3K_MOUSE KV1T_HUMAN KV1T_HUMAN KV1D_HUMAN KV1D_HUMAN KV1D_HUMAN KV1D_HUMAN KV1I_HUMAN KV3I_HUMAN KV3I_HUMAN KV3I_HUMAN	ALIGNMENT	PRT; ) quence notatio		., Ruti human g ain.";	t; nan	TI). 703; nabe S. The pri pa-type cid sed duction em. 353	818; n J.G., immuno nctiona	TTEIN ROY).  "U., Hess M. "L., Watanah (eds.); e and functi TTEIN CUM). 5586923;
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426 426 425 421 421 421 419 418.5 418.5 418 418 418.5		1 HUMAN 34; JL-1986 JL-1986 CT-2001	sapi ryota alia; Taxi	UENCE (MY LINE=7106 tlieb P.L e covalen d sequenc	121 MEDILEIDE BONDS. MEDILINE=71064027; PubMed=492314. Gall W.E., Edelman G.M.; "The covalent structure of a hu Intrachain disulfide bonds."; Biochemistry 9:3188-3196(1970).	UENCE (BE LINE=7218 er L., Ba le of ant unoglobul . IV. The mechanis	SEQUENCE FROM N.A. MEDLINE-81042304; Pubme Hieter P.A., Max E.E., "Cloned human and mouse genes conserve homology cell 22:197-207(1980).	CE man glock transport to the contract transport transpo
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-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
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Wataryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein."
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3550(1969).
                                                                                                                                                                                                              MEDLINE-70201507; PubMed-5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FIId=VAR_003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

W; 51984DIFDD372CE8 CRC64;
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region.
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721-JUL-1986 (Rel. 01, Last sequence update)

19-JUL-1999 (Rel. 38, Last annotation update)

19 kappa chain V-III region MOPC 63 precursor.
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                                          SEQUENCE (BENCE-JONES PROTEIN AG)
                                                                MEDLINE-69234734; PubMed-4893682;
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57 E
11609 MW;
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PROSITE; PS00290; IG_MHC; 1.
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Matches 106; Conservative
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106
83
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P01661;
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DISULFID
VARIANT
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MEDLINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                             SEQUENCE OF 21-131.
MEDLINE=73140225; PubMed=4691517;
MCKean D.3., Potter M., Hood L.E.;
"Mouse inmunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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                                                Burstein Y., Schechter I.;
"Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVMSM6.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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SMART, SM0406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
SEQUENCE OF 1-35.
MEDLINE=78235887; PubMed=98179;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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|121 TFGGGTKLEIK 131
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Best Local Similarity
Matches 98; Conserv
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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Pred. No. 2.7e-32;
9; Mismatches 11;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-III region PC 7183.
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                                                                                                                                                                                                                                                                                                                                             111
12002 MW;
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Nature 276:785-790(1978).
PIR; BO1937; KVMS93.
HSSP; PO1789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_v.
Fran; PF00047; ig; 1.
SWART; SM00406; IGv.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                39.1%;
82.0%;
                                                                      PIR; A01937; KVMS43.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMARF: SM00406; IGv: 1.

DOMAIN 24 38

DOMAIN 24 38

DOMAIN 54 60

DOMAIN 61 92

DOMAIN 61 92

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DOMAIN 93 101

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Nature 276:785-790(1978).
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P01666;
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SEQUENCE
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KV3N_MOUSE
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                                                                                                                                                                                                                                                                Biochemistry 12:749-759(1973).
-!- MISCELLANGOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
BENCE-JONES PROPEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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MEDILINE-73140234; PubMed-4120629;
MECRAIN D. J., POLTER M., HOOd L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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COMPLEMENTARITY - DETERMINING - 3
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; Signal.
SIGNAL 1 20
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 7043.
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              SEQUENCE OF 1-37.
MEDLINE=78235887; Pubmed=98179;
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HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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121 TFGSGTKLEIKR 132
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132
132 AA;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                        ;
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FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-1.
                                                     COMPLEMENTARITY-DETERMINING-2.
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sapiens (Human).
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                                                       1 DIVLIQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                             21 DIVLTQSPSSLSASVGDRVT_ITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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       Length 111;
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Pred. No. 5.5e-32;
9; Mismatches 12; Indels
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                          11; Indels
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       Score 482; DB 1;
Pred. No. 3.8e-32;
                                                                                                                                                 FY30_MOUSE STANDARD; PRT; 111 AA. P01667; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-III region PC 6308.
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                          10; Mismatches
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BY SIMILARIT
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12071 MW;
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PIR; C01937; KVMS08.

HSSP; P01789; 1MCP.

InterPro; IPR003006; Ig_MC.

InterPro; IPR003306; Ig_V.

Pfam; PF00047; Ig; 1.

Immunoq10bulin V region.
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81.1%;
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illarity 81.1%;
Conservative
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hes 90; Conservative
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61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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MEDLINE-88014148; PubMed-6091049;
KIObeck H.G., Combriato G., Zachau H.G.;
Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
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Autoantibody-associated kappa light chain variable region gene
"Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somat:
mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-!- DISEASE: THE ROPEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBOTHES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
     Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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JKI SEGMENT.
BY SIMILARITY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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13.40G-1987 (Rel. 05, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
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Homo sapiens (Human),
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HSSP, P01789; LINCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam; PP0047; 19; 1.
SMART; SM00406; IGV.
Immunoglobulin V region; Signal.
                                                                                                                                                  MEDLINE=88171307; PubMed=3127527;
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129 AA;
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FRAMEWORK - 1

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Mus musculus
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P01664;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                          IG KAPPA CHAIN V-I REGION WALKER.
                                                                                                                                                                                                                                                                                                          Query Match 38.7%; Score 479; DB 1; Length 129; Best Local Similarity 73.3%; Pred. No. 8.1e-32; Matches 96; Conservative 13; Mismatches 18; Indels
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region PC 7769.
Mus musculus (Mouse).
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                                                                               EMBL; X00965; CAA25477.1; ALT_TERM.
                                                                                         PIR; A01883; KIHUWK.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv.; Immunoglobulin V region; Signal.
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PIR; E01937; KWMS69.
HSSP; P01789; IMCP.
INTERPO; IPR003006; Ig_MHC.
INTERPO; IPR003596; Ig_V.
Ffan; FF00047; Ig, I.
SWART; SM00406; IGV; I.
Immunoglobulin V region.
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129 AA;
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MCKean D.J., Bell M., Potter M.;

McCon Math., Potter M.;

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELONA PROTEIN.

HSPP, P01789; INCP.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_V.

Pfam; PF000047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVLIQSPASLAVSLGQRATISCKASQSVDYTGESYMNWYQQNPGQSPKLLIYAASNLES 60
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                               81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                    81 GIPSRESGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                                                                               38.6%; Score 477; DB 1; Length 111; 80.2%; Pred. No. 9.6e-32; ive 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%; Score 469; DB 1; Length 111; 79.3%; Pred. No. 4.2e-31; Indels ive 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING-1.
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FRAMEWORK-4.
                COMPLEMENTARITY-DETERMINING-1.
                                                       COMPLEMENTARITY - DETERMINING - 2.
                                                                                               COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                                         6FAA345279356829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CBPC 101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 111 AA
                                                                                                                                    BY SIMILARITY.
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                                                                              FRAMEWORK - 3
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                                                                                                                  FRAMEWORK - 4
                                                                                                                                                                         12011 MW;
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Best Local Similarity
Matches 89; Conserv
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KV1H\_HUMAN

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21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic nutation. Implications for etiology and immunotherapy.";

T. Exp. Med. 167:840-852(1988).

-I. DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                          COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                                                                                                                                                         69F1A5CE886B1249 CRC64;
                                                                                                                                                                                                                                                                                                                                37.1%; Score 459.5; DB 1;
79.3%; Pred. No. 2.4e-30;
iive 10; Mismatches 12;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
II g kappa chain V-III region HIC precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                            BY SIMILARITY.
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                                                                                                                                                                                                                                                                                         11950 MW;
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HSSP; PLO189; IMCP.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
Immunoglobulin V region; Signa SIGNAL 1 22 129 If DOMAIN 21 129 If DOMAIN 21 43 FF DOMAIN 56 70 FF DOMAIN 71 77 CC DOMAIN 71 77 CC
                                        Nature 276:785-790(1978).
PIR; D01937; KVMS10.
HSSP; P01789; 1MC2P.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                 Pfam; PF00047; ig; 1. SMART; SM00406; iGv; 1. Immunoglobulin V region.
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Best Local Similarity
Matches 88; Conserv
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P18136;
                               diversity.
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KV3M_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
                                                                                                                                                                                                                                                         MEDLINE-71032830; PubMed-4097974; Watanabe S., Hilsenhann N.; Watenabe S., Hilsenhann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                       Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.2%; Score 460; DB 1; Length 108; 79.5%; Pred. No. 2.1e-30; Live 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08D3A6160D8D0618 CRC64;
                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Hau.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin V region; Bence-Jones protein.
                                                                                     108 AA
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BY SIMILARITY.
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SEQUENCE.
MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11671 MW;
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                                                                                     STANDARD;
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P01668;
                                                                                     KV1H_HUMAN
P01600;
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Best Local Si
Matches 899
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RESULT 12 KV3P\_MOUSE

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Length 110;

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                                                                                                                                                                                              MEDLINE-75059122; PubMed-4215718;
Laure C.J., Watanabe S., Hilschmann N.;
Laure Primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).

-i. MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-i. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                            Gaps
                                                                                                                                 1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                               4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Hómo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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M
                                                                                Query Match 37.0%; Score 457.5; DB 1; Length 129; Best Local Similarity 68.2%; Pred. No. 4.2e-30; Matches 90; Conservative 16; Mismatches 23; Indels 3
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
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                                               MW; 7395528EA2BB74D6 CRC64;
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Pred. No. 1.1e-29;
                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region GAL.
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BY SIMILARITY.
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PIR; A01867; KIHGEL.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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78.6%;
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Best Local Similarity 78.6
Matches 88; Conservative
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129 AA;
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P01599;
        DOMAIN
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KV1G_HUMAN
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Capra J.D., Klapper D.G.;

"Complete amino acid sequence of the variable domains of two human
"Complete amino acid sequence of the variable domains of two human
"Complete amino acid sequence of the variable domains of two human
"The minion of the sequence of the variable didotypic
"The search J. Immunol. 5:677-684(1976)"
"The minion of the second and the buman pow V-III Kappa CHAIN.
"The MICHILANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
"THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
"THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
"THE SECOND AND THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
"PIR'S AOUGH, KINDLY.
"PROBLEM OF THE SECOND AND THE HYPERVARIABLE REGIONS OF THIS
"THE SECOND AND THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
"PIR'S AOUGH, KINDLY.
"PROBLEM OF THE SECOND AND THE HYPERVARIABLE REGIONS OF THIS
"THE SECOND AND THIS CHAIN.
"THE SECOND AND THIS CHAIN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2%; Score 448; DB 1;
illarity 77.7%; Pred. No. 1.9e-29;
Conservative 9; Mismatches 12;
                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Lay.
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                                                                                                                                                              STANDARD;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Database

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### ALIGNMENTS

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	Description	Q99m37 mus musculu	Q91wf8 mus musculu	Q91ws9 mus musculu	Q9rla5 mus musculu	O91w12 mus musculu	Q91x10 mus musculu	Ogul77 homo sapien	096sa9 homo sapien	Q9ul70 homo sapien	Ogul81 homo sapien	Q9ul79 homo sapien	Q96pf6 homo sapien	Q99m11 mus musculu	Q96e61 homo sapien	O920e9 mus musculu	Q9ul78 homo sapien
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SUMMARIES	q:	Q99M37	Q91WF8	Q91WS9	Q9R1A5	Q91W12	Q91XL0	Q9UL77	Q96SA9	Q9UL70	Q9UL81	Q9UL79	Q96PF6	Q99M11	Q96E61	Q920E9	09UL78
	В	11	11	11	11	11	11	4	4	4	4	4	4	1	4	11	4
	Query Core Match Length DB II	238	234	233	214	235	211	108	107	108	107	108	116	235	236	111	109
,	% Query Match	60.3	59.7	59.6	58.5	57.0	56.8	38.0	37:4	36.3	35.4	35.2	34.9	34.8	34.6	33.5	32.0
	Score	745.5	738	737	724	704.5	703	470	462.5	449	437.5	436	432	430.5	428	414	395.5
	Result No.	1	2	e	4	S	9	7	ω	6	10	11	12	13	14	15	16

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Gaps

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Query Match 60.3%; Score 745.5; DB 11; Length 238; Best Local Similarity 58.1%; Pred. No. 9.1e-58; Aatches 136; Conservative 41; Mismatches 56; Indels 1;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*

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SEQUENCE FROM N.A.
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                                                                                                                  65 GQSPKLLIXKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGS 124
                                                                                                                                                                                 125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 184
                                                                                                                                                                                                        65 GKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
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01-DEC-2001 (TEXMBLrel. 19, Created)
01-DEC-2001 (TEXMBLrel. 19, Last sequence update)
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                             181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 234;
                                                                                                                                                                                                                                                                     185 ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ database EMBL; BC015292; AAH15292.1; -- Hypothetical protein. SEQUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    091MFB;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.7%; Score 738; DB 11;
59.7%; Pred. No. 4.1e-57;
ive 34; Mismatches 58;
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Best Local Similarity 59.78
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1199) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI52371; AAD40242.1;
HSSP; P01679; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                         11 LLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKL 70
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                                                                                                                                                                                                                                                                                                                                                                                                                   10 LLLCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSQGI----ANYLNWYQQKPDGTVKL
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                 Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 233
                                                                                                                                                                                                                                                                                                        Indels
                                                      the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                              59.6%; Score 737; DB 11;
62.7%; Pred. No. 4.9e-57;
live 29; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.5%; Score 724; DB 11; 62.8%; Pred. No. 6.1e-56; ive 31; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00290; IG_MHC; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003600; Ig_like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 2
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23922 MW;
TISSUE-COLON;
Strausberg R.;
Submitted (SEP-2001) to the E
EMBL; BC013496; AAH13496.1; -
Hypothetical protein.
NON_TER
                                                                                                                                                                                                                                                                              Best Local Similarity 62.7%
Matches 143; Conservative
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Matches 137; Conservative
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200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                             141 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.0%; Score 704.5; DB 11; Length
60.6%; Pred. No. 3.6e-54;
Live 32; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643; AAH06643.1; -.
SEQUENCE 235 AA; 26021 MW; SFC73BDEBD5EBFEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -.
?: SFC73BDEBD5E8FEF CRC64;
                                                                                                                                                                                                                                                                                       091W12 PRELIMINARY; PRT; 235 AA. 091W12; U-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) UNKNOWN (PROTEIN FOR MGC:6582).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=KIDNEY;
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Mammalia; Eutheria; Rodentia;
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Matches 134; Conservative
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TISSUE=BREAST TUMOR;
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Q91XL0
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STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE=20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
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                       Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sano H., Saski D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T., Soqabe Y., Suzuki H., Taqami M., Taqawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yasunishi A., Yoshino M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/60; TISSUE-KIDNEY;
MEDLINE-20530913; PubMed=11076861;
Shibata K., Ttoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Ttoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yuneda Y., Ishikawa T., Ozawa W., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
EMBL; AKO02514; BAB22154.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM CONSOrtium.;
"Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 4.2e-54;
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MEDLINE-99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
Carificiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
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Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                           'Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                         81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 36.3%; Score 449; DB 4; Length 108; 1 Similarity 77.7%; Pred. No. 3.8e-32; 87; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09UL81;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                         81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11633 MW; B7BEDC3E41FCCA37 CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; IREI.
INTEPPRO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGy: 1.
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MEDLINE-98277139; PubMed~9614934;
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                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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Matches 87; Conserv
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108 A
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                                                                                                                   Euteleostomi;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin_reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-NYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
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SEQUENCE FROM N.A.
MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin rheumatic carditis:""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 462.5; DB 4; Length 107;
Pred. No. 2.4e-33;
7; Mismatches 7; Indels 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 470; DB 4; Length 108; Pred. No. 5.4e-34;
                          01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                        108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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                                                                                                                                                                                                                                              fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD3607; AAD56273.1;
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
 108 AA
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J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%;
82.1%;
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83.08;
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 PRELIMINARY;
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                                                                                                  Homo sapiens (Human).
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107 AA;
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Best Local Similarity
Matches 93; Conserv
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                                                                                                                                           NCBI_TaxID=9606;
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01-DEC-2001
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ID Q96PF6
                     096PF6;
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                                                                                                                                                                                      4; Gaps
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
Myosin-reactive autoantibodies in rheumatic carditis and normaletus.",
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                                                                                                                                                                                                                  81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                           Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.2%; Score 436; DB 4; Length 108; Best Local Similarity 76.8%; Pred. No. 5.3e-31; Matches 86; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                          Indels
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107 AA; 11501 MW; 070549FDE0754748 CRC64;
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                                                                                                                                    Query Match 35.4%; Score 437.5; DB 4; Best Local Similarity 77.7%; Pred. No. 3.9e-31; Matches 87; Conservative 10; Mismatches 10;
                  Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
NON_TER.
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EMBL; AF035035; AAD56271.1; -
HSSP; P01607; IREI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                      108 AA
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SMART; SM00406; IGV; 1.
NON_TER 108 108
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Q9UL79
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81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJUNE-21361171; PubMed-11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell burden."; Blood 98:714-720(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.9%; Score 432; DB 4; Length 116; 70.0%; Pred. No. 1.3e-30; Live 15; Mismatches 17; Indels
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL: BC002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
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116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
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                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA I LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.4 KDA PROTEIN.
116 AA.
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InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_11ke.
InterPro; IPR003600; Ig_11ke.
InterPro; IPR003600; Ig_NHC.
InterPro; IPR003596; Ig_V.
SMART; SM00409; IG; 2.
SMART; SM00400; IG; 2.
SMART; SM00410; IG_1; 1.
SMART; SM00410; IG_1; 1.
SMART; SM00410; IG_1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
HYPOTCHetical Protein.
SEQUENCE 235 AA; 25403 MW; 39807BFF
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                                                                                                                                                                                                125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 APKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ--QSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGN 182
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                                                                          6 LLLVFLHHLTGSCAQLVLTQ-PSSVSTSLGSTAKLPCKA--STGNIGDSYVNWYQQYMGR 62
                        Gaps
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                                                                                                                                                                                                                                                                      184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                            180 QGVETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234
                                                     7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LLMVLLLMVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-MIMICKING ANTI-IDIOTOPE RAPPA CHAIN VARIABLE REGION
   Pred. No. 4.5e-30;
3; Mismatches 86; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg R.;
Straubberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;
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TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) UNKNOWN (PROTEIN FOR MGC:17259).
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41.9%; Pred. No. 7.4e-30;
Live 40; Mismatches 87;
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Best Local Similarity 42.2
Matches 100; Conservative
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Search completed: August 14, 2002, 15:22:15 Job time: 683 sec

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Gaps
                                              SEQUENCE FROM N.A.
Atkin J.D., lape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
                                                                                                                                                                                                                                                                                                              21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                1 DIVLIQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60
Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                             Submitted (SEP-2000), to the EMBL/GenBank/DDBJ databases EMBL, AF307935; AAL09419.1; -. 1 1 1.1 1.1 1.1 SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;
                                                                                                                                                                                                                                          33.5%; Score 414; DB 11;
illarity 71.2%; Pred. No. 4.7e-29;
Conservative 13; Mismatches 19;
                                                                                                    in Mammalian Cells.";
 Mammalia; Eutheria;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:01:42 ; Search time 230.21 Seconds (Without alignments) 38.599 Million cell updates/sec Run on:

2\_G\_3\_G\_4 246 1 SYWMQXXXXXXXXXXXXXXXE.....XXXXXXXXXNRDYSNNWYFDV 80 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

747574 seqs, 111073796 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_032802:\* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Anti-Fas humanised	Fragment of humani	Humanised anti-Fas	Anti-Fas MAb HFE7A	Mouse anti-Fas ant	Murine anti-Fas an	Anti-Fas humanised	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Humanised HFE7A de
		O O	AAW83038	AAB14775	AAW90925	AAW83041	AAB14747	AAW90897	AAW83036	AAW83037	AAB14776	AAB14779	AAW90926
		DB	19	21	21	19	21	21	19	19	21	21	21
		Watch Length DB ID	145	145	145	464	464	464	470	470	470	470	470
dР	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	246	246	246	246	246	246	246	246	246	246	246
	Result	No.	1	7	3	4	2	9	7	8	6	10	11

Humanised HFE7A de Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Humanised HFE7A de	Anti-EGFR antibody Anti-DNA antibody Anti-DNA antibody Anti-DNA antibody Anti-DNA antibody	Murine 19BB neavy Anti-DNA antibody SNV-env leader/hum ScFv(FWP51). Synt FWP51 fusion prote (FRP51)-ETA fusion Anti-DNA antibody	Protein sequence o Murine Act.1 heavy Consensus protein Heavy chain of a h Murine 66425 heavy Humanised murine 6 Humanised murine 6	Murine 6G425 heavy Humanised 6G425 F( Single chain Fv an Anti-9p54 MAD T16 Anti-9p54 MAD T16 Monoclonal antibod Anti-IL-8 MAD 6G4. Anti IL-8 Antibody Anti IL-8 Antibody Anti IL-8 Ancoclon
AAW90929 AAW90933 AAW90934 AAW90935 AAW90936		AAY92156 AAW04590 AAB70841 AAR85495 AAR26981 AAR26983 AAW04588		AAY77753 AAB70764 AAB70762 AAW26800 AAY27074 AAY2322 AAW42322 AAW42322
21 21 21 21 21	4 2 8 8 8 8	21 22 22 13 13 13	110 110 110 110 110 110 110 110 110 110	221 221 221 230 138 188
470 470 470 470	111	111 309 240 241 637	137 144 180 1117 1117	117 262 262 119 245 125 135 135
100.0 100.0 100.0 100.0	ппооб	655.0 64.2 64.0 64.0 64.0 63.8	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	633.0 622.0 622.2 602.2 600.0 600.0
246 246 246 246 246	176 176 164 164	161 160 158 157.5 157.5 157.5	156 156 156 155 155 155	155 155 154 153 148.5 147.5 147.5
12 13 14 15	118 119 20 210	22222222222222222222222222222222222222	. 332 332 334 334 334	788844444 788844444 78888

#### ALIGNMENTS

AAW83038 standard; Protein; 145 AA 15-MAR-1999 (first entry) AAW83038; AAW83038 RESULT 

Anti-Fas humanised antibody HFE7A heavy chain variable region.

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; slogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Homo sapiens. Synthetic.

Socation/Qualifiers Peptide Protein Region

Region

SEQ ID NO:75.

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Fragment of humanised anti-Fas antibody heavy chain,
                                                                                                                                                          JP2000169393-A.
                                                                                                                                                                                                         30-SEP-1999;
                                                                                                                                                                                                                                30-SEP-1998;
                                                                                                                                                                                   20-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the VD type humanised heavy chain variable region of murine anti-human Fas monoclonal antibody HFETA. It was utilised in a claimed humanised HFETA heavy chain (see AAV70079). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFETA (see AAW83031-37) are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. Humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Slogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's alsease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, ampocarditis, cardiomyopathy, glomecular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                   Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.4e
46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 207; 292pp; English.
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/label= CDR_H2
/note= "claim 9"
118..129
/label= CDR_H3
/note= "claim 9"
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97JP-0169088.
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                                                                                                                                                                                                                   Akio S, Hideyuki H,
Masahiko O, Nobufusa
                                                                                                                                                                                             (SANY ) SANKYO CO LTD.
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Best Local Similarity
                                                                                                                                                                                                                                                     WPI; 1998-543440/47.
N-PSDB; AAV70104.
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                                                                                                                      30-MAR-1998;
                                                                                                                                             08-OCT-1997;
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                                                                                                                                                                    25-JUN-1997;
                                                                      AU9859701-A
                                                                                              08-OCT-1998
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                          Region
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14775-B14776 and ABB14779 represent the heavy chains (or fragments thereof) of various humanised
Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand, apoptosis modulator; programmed cell death; autoinmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
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1.4e-11;
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42.5%; Pred. No. 1.4e-11;
tive 46; Mismatches 0;
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                                                                                                                                                                                                                                               Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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N-PSDB; AAA72146.
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Best Local Similarity
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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
capoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
canti-anemic, antidiabetic, anti-alergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
cantiartroisoclerofic, cardiant and hepatropic activity. (I) induce
antiarteriosoclerofic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competition
canemia, Addison's disease, sloraderma, Goodpasture syndrome, Crohn's
disease, autoinmune hemolytic anemia, sterility, myasthenia gravis,
calendar, Addison's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
conflicting a human anti-murine antibody response. This sequence represents
can humanised anti-marine antibody HERSA heavy chain which is used in
cut the method described in the invention.
                    anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; demachological; lamunosuppressive; thyrominetic; antirhematic; antirhematic; antirhematic; antirhematic; antirhematic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimcto disease; praft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; myasthenia gravis; multiple sclerosis; basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o anti-Fas antibody, useful for treating or preventing e.g. or autoimmune disease, induces apoptosis selectively in
  antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-Fas antibody, useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example reference 15; Page 126-127; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                    99EP-0307711
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                                                                                                                                                                                                                                                                                        Synthetic.
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0
   Score 246; DB 21; Length 145;
                                  Indels
                 1.4e-11;
                ; Pred. No. 1.46
46; Mismatches
100.08;
                   42.5%;
 Query Match
Best Local Similarity 42.5
Matches 34; Conservative
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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                    apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pennicious anaemia; Addison's disease; Schortoderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
                                                                                                                                                                             monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                      label- Sig_peptide
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                AAW83041 standard; Protein; 464 AA.
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69..84
                                                                                                                                                                                                                                                                                                                                                                                                                             'label- Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                       141..464
/label= Constant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= CDR_H3
/note= "claim 9"
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                                                                                                                                                    Anti-Fas MAb HFE7A heavy chain.
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/label= CDR_H1
            61 XXXXXXXXNRDYSNNWYFDV 80
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97JP-0169088
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                                                                                                                                                                                                                                                                                                                                 Mus musculus.
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                                                                     AAW83041
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WPI; 2000-258930/23.
N-PSDB; AAA11546.
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                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                       Query Match
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                             This is the amino acid of the heavy chain of murine anti-human Fas chain was obtained from HFE7A-screting hybridoma (FERM BP-5828)

KNA by RT-PCR (see AAW83031-37) produced by CDR graffing.

RNA by RT-PCR (see AAW83031-37) produced by CDR graffing. These antibodies (see AAW83031-37) produced by CDR graffing. These artibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting reas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's diseases (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, solercoderma, Goodpasture syndrome, Crohn's disease, themmatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia and insulin-dependent diabetes). Allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             murine; complementarity determining region; CDR; human Fas;
Fas ligand; apoptosis modulator; programmed cell death;
autoimmune disease; allergy; atcopy; arteriosclerosis; myocarditis;
cardiomyothy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 246; DB 19; Length 464; Local Similarity 42.5%; Pred. No. 3.9e-10; Los 34; Conservative 46; Mismatches 0; Indels 0;
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          Reference Example 4; Page 187–188; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse anti-Fas antibody HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14747 standard; Protein; 464 AA.
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                                                                                                                                                                                                                                                                 464 AA;
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                                                                   The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arterfosels, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS heavy chain of the murine anti-human Fas monoclonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 246; DB 21; Length 464; 42.5%; Pred. No. 3.9e-10; Live 46; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine anti-Fas antibody HFE7A heavy chain protein.
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Example 4; Page 67-68; 139pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW90897 standard; Protein; 464 AA.
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Matches 34; Conserv
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Homo sapiens.

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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
capoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
canti-anemic, antidiabetic, anti-alergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
cantiartriosclerofulc, cardiant and hepatropic activity. (I) induce
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
cantiartriosclerofulc, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by systemic
lugus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Slorgem s syndrome, pernictous or hypoplastic
canemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoinmune hemolytic anemia, sterility, myasthenia gravis,
cardiomyopathy, glomerulonephritis, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejectively induce it na abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
cultine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
cannic and an anti-marine antibody response. This sequence represents
cannic and a successive and antibody response. This sequence represents
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               New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; actoriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 246; DB 21; Length 464;
Pred. No. 3.9e-10;
Mismatches 0; Indels 0
                                                                                                                 Example reference 4; Page 100-102; 263pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 100.0%; Score 246; C
Local Similarity 42.5%; Pred. No. 3.9e
hes 34; Conservative 46; Mismatches
                                                                   cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW83036 standard; Protein; 470 AA.
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chain of murine anti-human Fass monoclonal antibody HFE7A. E. coll pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion of fragment of the humanised vor type HFE7A heavy chain and DNA encoding human 1gG1 constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised to versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sjögren syndrome, pernicious anaemia, Addison's disease, scleroderma Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the VD type humanised heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
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                                                          ..19
|abel= Sig_peptide
                                          location/Qualifiers
                                                                                    0..470
label- Mat_protein
                                                                                                                20..140
/label= Variable
                                                                                                                                                                                                      /note= "claim 9"
69..84
                                                                                                                                              41.464
Tabel Constant
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/note= "claim 9"
118..129
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/note= "claim 9"
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/label= CDR_H1
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97JP-0169088
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25-JUN-1997;
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            Synthetic.
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                                                         Peptide
                                                                                       Protein
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DB 19; Length 470;

100.0%; Score 246;

Query Match

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JP2000169393-A.
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                                          50 sywmqwvkqapgqrlewmgeidpsdsytnyngkfkgkatltvdtsastaymelsslrsed 109
             Gaps
                           SYWMQXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                               apoptosis: HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sigogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
                                                                                                                                                                                      HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                     myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; actopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                rheumatoid arthritis; autoimmune haemolytic anaemia;
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Tohru T;
   Pred. No. 4.1e-10; imismatches 0
                                                                                                                                                                     Anti-Fas humanised antibody HFE7A heavy chain.
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Masahiko O, Nobufusa S, Shin Y, Tohru
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/label= Sig_peptide
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/label= Mat_protein
                                                                                                                    AAW83037 standard; Protein; 470 AA.
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/label= Variable
42.5%; Pre
                                                                                                                                                                                                                                                                                                                                                                                  Constant
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/label= CDR_H1
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR_H2
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                                                                     110 tavyycarnrdysnnwyfdv 129
                                                            61 XXXXXXXXNRDYSNNWYFDV 80
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97JP-0082953.
97JP-0169088.
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                                                                                                                                                      (first entry)
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          118..129
/label= C
                                                                                                                                                                                                                                                                                                                                                                          41..464
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   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV70080
                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                     15-MAR-1999
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                                                                                                                                     AAW83037;
                                                                                                                                                                                                                                                                                                                      Peptide
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           Matches
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This is the amino acid sequence of the HV type humanised heavy

chain of murine anti-human Fas monoclonal antibody HFE7A. It
includes humanishing R44G and A7GT anino acid substitutions that are
are conserved in the human Egg heavy chain. Host Escherichia coli
geHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion
fragment of the humanised HV type HFB7A heavy chain and DNA
encoding human 1gG1 constant region (see AAV70080), and is deposited
as FERW BP-6273 (claimed). The invention provides methods for
producing humanised antibodies by culturing host cells. Humanised
versions of HFE7A (see AAM83031-37), like native HFE7A, are capable
of inducing apoptosis in abnormal cells. The humanised
inhibiting Fas-induced apoptosis in normal cells. The humanised
antibodies are used to evaluate, in animal models, treatments of
diseases that involve FasyFas ligand interactions, and also to
treat such diseases, including autoimmune disease (e.g. systemic
lupus erythematosus, Hashimoto's disease, graft versus host disease,
Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
Goodpasture syndrome, Crohn's disease, thrombopenia purpura and
insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
multiple scl rosis, Bassedow's disease, thrombopenia purpura and
insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
anaemia, hepatitis, AIDS and transplant rejection (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 246; DB 19; Length 470;
Pred. No. 4.1e-10;
6; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
                                                                                                                                                                                                               Claim 22; Page 225-227; 292pp; English.
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42.5%; F. 46;
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Best Local Similarity
Matches 34; Conserv
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(SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA.

Complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, artery careforesis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; attopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                          Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
                                                                                                                                       Claim 21; Page 95-96; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14779 standard; Protein; 470 AA
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            98JP-0276883.
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Matches 34; Conservative
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                                  (SANY ) SANKYO CO LTD.
                                                        WPI; 2000-485645/43.
N-PSDB; AAA72159.
                                                                                                                                                                                                                                                                                                                                               470 AA;
                                                                                                                  anti-Fas antibody
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           30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to compositions for the prevention or treatment confidences caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
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                                                                                                                                                                                                                                                                               Claim 21; Page 108-109; 139pp; Japanese.
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WPI; 2000-485645/43.
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                                         N-PSDB; AAA72184
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                                                                                                                                                                                                                                                                                                                                          This invention describes a novel numanized anti-ras antibody. Tike molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas indecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas indecule (I) that, induces apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammetory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antidiabetic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent of iseases associated with the Fas/Fas ligand system, especially systemic upon system associated with the Fas/Fas ligand system, especially systemic unitiple sclerosis, disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoinmune hemolytic anemia, sterility, mysathenia gravis, anitiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fase, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic multiple abundand described in the invention; and sequence represents a humanised anti-Fas antibody HRE7A designed heavy chain which is used in the method described in the invention.
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                                                                                                                                                                                              New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                       Tamaki I, Takahashi T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                      Example reference 15; Page 134-136; 263pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.16
                                                                                                                                                                                                                                               cells with abnormal Fas-Fas ligand systems
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                                                                                       Nakahara K,
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98JP-0276882
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                                                                                       Serizawa N, Haruyama H,
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                                           (SANY ) SANKYO CO LTD.
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Matches 34; Conserva
                                                                                                                              WPI; 2000-258930/23.
                                                                                                                                                       N-PSDB; AAA11597
30-SEP-1998;
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apptosis in cells with a normal system, by inhibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between the products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, anti-anemic, nephrotropic, antimosuppressive, thyromimetic, antirheumatic, nephrotropic, antimosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce contribution of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic cubbition of ligand binding. (I) are used to treat and/or prevent disease, sjorgen's syndrome, pernicious or hypoplastic contains and system, especially systemic syndrome, pernicious or hypoplastic contains, and sistems, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral colls. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEFAA designed heavy chain which is used in the method described in the invention.
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hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example reference 22; Page 150-152; 263pp; English.
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98JP-0276882.
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Matches 34; Conserv
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88888g Qγ g ò This interior describes a novel numerized anti-ras antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by induces apoptosis in cells with an abnormal Fas/Fas ligand system, by indubling binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antalogical, immunosuppressive, thyromimetic, anti-anemic, antidiabetic, antinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce antiarteriosclerotic, cardiant and hepatropic activity. (1) induce antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic complexity host disease, soleroderma, Goodpasture syndrome, Crohn's disease, solorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, mycarditis, dependent diabetes mellitus, allergy, arteriosclerosis, mycarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B. C or D) or alcoholic), and transplant rejection. (1) selectively cells, they bind to both human and murine Fas, so can be evaluated in culling that apoptosis in normal cells fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; antialergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparctropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in This invention describes a novel humanized anti-Fas antibody-like Nakahara K, Tamaki I, Takahashi T; Humanised anti-Fas designed heavy chain Heu 1 protein. cells with abnormal Fas-Fas ligand systems Claim 2; Page 169-170; 263pp; English. AAW90933 standard; Protein; 470 AA 110 tavyycarnrdysnnwyfdv 129 99EP-0307711. 98JP-0276881. 98JP-0276882. (first entry) Haruyama H, (SANY ) SANKYO CO LTD. WPI; 2000-258930/23. N-PSDB; AAA11644 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; 08-AUG-2000 Serizawa N, EP990663-A2 Synthetic. AAW90933; AAW90933

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inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 1 which is described in the method of the invention.
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                                                                                                                                                                                                                                                          100.0%; Score 246; DB 21; Length 470;
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46; Mismatches
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98JP-0276882.
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30-SEP-1998;
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosolerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus extytematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Slorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
anitiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephitis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
chlibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
muning a human anti-murine antibody reaponse. This sequence represents
a humanised anti-Fas antibody heavy chain construct designated Heu 2.
which is described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 246; DB 21; Length 470; 42.5%; Pred. No. 4.1e-10; ive 46; Mismatches 0; Indels 0
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW90935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW90935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οp
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This invention describes a novel numerized anti-ras antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas [igand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive confibilition of ligand binding. (I) are used to treat and/or prevent clipsus erythematosus, Hashimoto disease, rheumatoid arthritis, graft diseases associated with the Fas/Fas ligand system, especially systemic clipus erythematosus, Hashimoto disease, rheumatoid arthritis, graft oversus host disease, solorgen's syndrome, periodicus or hypoplastic anemia, Addison's disease, solorgen's syndrome, periodicus or hypoplastic anemia, Addison's disease, solorgen's syndrome, periodicus or hypoplastic anemia, Addison's disease, solorgen's syndrome, periodicus or hypoplastic cardiomyopathy, glomerulonephitis, therefore syndrome, Confidence in the molytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively (B, C or D) or alcoholic), and transplant rejection. (I) selectively chinate disease models. (I) act on the active site of Fas, i.e. they mimic cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic a human anti-murine antibody heavy chain construct designated Heu 3 munualised anti-Fas antibody pasy chain construct designated heu 3 
                                                                                                          New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 246; DB 21; Length 470; 42.5%; Pred. No. 4.1e-10; ive 46; Mismatches 0; Indels 0
                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                    Claim 2; Page 180-182; 263pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.5%
Matches 34; Conservative
                        WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.0 AA;
                                                      N-PSDB; AAA11646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
a
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61 XXXXXXXXNRDYSNNWYFDV 80 οχ

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110

Search completed: August 14, 2002, 15:15:33 Job time: 831 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:05:37; Search time 82.88 Seconds (without alignments) 23.577 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table:

231628 seqs, 24425594 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

231628

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/laa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/laa/pCTUS\_COMB.pep:\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		•			SUMMARIES	
Result	Score	Query	* Query Match Lenath DR	a c	£	Description
				1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
1	176	71.5	119	7	-08-523	Sequence 8, Appli
2	176	71.5	119	7	553	Sequence 12, Appl
m	164	66.7	111	m	US-08-881-037-14	14,
4	164	66.7	111	m	US-08-881-037-16	16,
S	164	66.7	119	m	US-08-881-037-61	61,
9	164	66.7	119	m	US-08-881-037-62	62,
7	160	65.0	111	m	US-08-881-037-17	17,
80	160	65.0	119	m	US-08-881-037-63	63,
σ	159	64.6	86	m	US-08-881-037-59	59,
10	157.5	64.0	241	Н	US-08-235-838-11	11,
11	157.5	64.0	241	7	US-08-465-473B-11	11,
12	157.5	64.0	637	H	US-08-235-838-16	16,
13	157.5	64.0	637	7	US-08-465-473B-16	16,
14	157	63.8	111	m	US-08-881-037-15	15,
15	157	63.8	119	က	US-08-881-037-60	9
16	155	63.0	117	'n	US-09-027-449-48	48,
17	155	63.0	117	٣	US-09-027-449-49	49,
18	155	63.0	117	m	US-08-804-444A-48	4
19	155	63.0	117	m	US-08-804-444A-49	49,
20	155	63.0	117	4	US-09-026-985-48	4
21	155	63.0	117	4	US-09-026-985-49	49,
22		0.09	135	-	US-08-398-613A-50	50,
23		0.09	135	Н	US-08-398-612A-50	50,
24		0.09	135	-	US-08-398-611A-50	50,
25	147.5	60.0	135	~	US-08-491-334A-50	50,
26		0.09	135	m	US-09-027-449-37	37,
27	147.5	0.09	135	m	US-08-804-444A-37	37,

Appl								Appl			Appl						
Sequence 37,	Sequence 58,	Sequence 58,	Sequence 58,	Sequence 58,	Sequence 44,	Sequence 52,	Sequence 55,	Sequence 44,	Sequence 52,	Sequence 55,	Sequence 44,	Sequence 52,	Sequence 55,	Sequence 70,	Sequence 70,	Sequence 60,	Sequence 60,
US-09-026-985-37	US-08-398-613A-58	US-08-398-612A-58	US-08-398-611A-58	US-08-491-334A-58	US-09-027-449-44	US-09-027-449-52	US-09-027-449-55	US-08-804-444A-44	US-08-804-444A-52	US-08-804-444A-55	US-09-026-985-44	US-09-026-985-52	US-09-026-985-55	US-09-027-449-70	US-09-026-985-70	US-09-027-449-60	US-08-804-444A-60
4	Н	-	Н	~	m	m	m	m	m	c	4	7	4	m	4	m	(*)
135	253	253	253	253	253	253	253	253	253	253	253	253	253	256	256	298	298
60.0	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	60.0	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09
147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5

# ALIGNMENTS

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linear

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amino acid
                       TOPOLOGY:
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                                                                                                                                                                                                                                                                     11 SYMMHWYRQRPGGGLEWIGEIDPSDSYTHYNQKFRGKATLTVDKSSNTAYMQLSSLTSED 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ADAM, JANDES
APPLICANT: ADAM, JANDES
APPLICANT: ROSELL, ELISABET
APPLICANT: ROSELL, ELISABET
APPLICANT: ROSELL, ELISABET
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                            Query Match 71.5%; Score 176; DB 2; Length 119; Best Local Similarity 31.6%; Pred. No. 8.1e-07; Matches 25; Conservative 50; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/05/53,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 503
PRIOR BATE: 17-NOV-1995
PRIOR BALICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR.1995
PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 17-MAR.1994
PRIOR APPLICATION NUMBER: EP 94118970.6
FILING DATA: APPLICATION NUMBER: BP 94118970.6
FILING DATE: NO-DEC-1994
ATONNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33, 2022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08553497A Patent No. 5844093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KETTLEBOROUGH, C. A
BENDIG, MARY M.
ANSELL, KEITH H.
GUSSOW, DETLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     91 SAVYYCARS-DYGSS-HFD 107
                                                                                                                                                                                                                                                                                                                                                            61 XXXXXXXXNRDYSNNWYFD 79
                     : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 amino acids
SEQUENCE CHARACTERISTICS
                                                                                 MOLECULE TYPE: protein
                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-08-553-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                            TOPOLOGY:
                                                                                                           US-08-553-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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Gaps
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                                                                                               Length 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION UNMER: US/08/481,540
PILOR APPLICATION NUMBER: US/08/443,540
APPLICATION NUMBER: US/08/443,540
CLASSIFICATION S30
ATTORNEY/AGBNT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 203442110710
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION OF 913-5600
TELEPONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 164; DB 3; I
30.0%; Pred. No. 7.7e-06;
tive 46; Mismatches 3;
                                                                                          Query Match 71.5%; Score 176; DB 2; Best Local Similarity 31.6%; Pred. No. 8.1e-07; Matches 25; Conservative 50; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GAPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-881-037-14; Sequence 14, Application US/08881037; Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                    91 SAVYYCARS-DYGSS-HFD 107
                                                                                                                                                                                                                                                                                        61 XXXXXXXXNRDYSNNWYFD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 30.09
Matches 21; Conservative
; MOLECULE TYPE: protein US-08-553-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1018
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Length 119
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
                                                                                                                                                                                        COMPUTER: IBM PC_COMPATIBLE
COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 66.7%; Score 164; DB 3; 1
Best Local Similarity 30.0%; Pred. No. 9.5e-06;
Matches 21; Conservative 46; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
TILLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & FOEISTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                          ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 SAVYYCAKGR 100
                                                                                                       COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 XXXXXXXXNR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304-1018
                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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US-08-881-037-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 164; DB 3; Length 11
30.0%; Pred. No. 7.7e-06;
Live 46; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                          Sequence 16, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
APPLICANT: Swanson, Patrick C.
APPLICANT: APPLICANT: 1 Swanson, Patrick C.
APPLICANT: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: KONSKi, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-881-037-16
61 XXXXXXXXNR 70
                                       83 SAVYYCAKGR 92
                                                                                                                                                                                                                                                                                                                                                               Palo Alto
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                                                                                                       RESULT 4
US-08-881-037-16
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US-08-881-037-61
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                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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Gaps
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                                                                                                                                                                                   Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNATE: CA
CUMTARY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUW TYPE: FILIPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION 530
PRIOR APPLICATION BTA:
APPLICATION NUMBER: 18 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KOORKI, Antoinette F.
REGISTRATION NUMBER: 34,2021,310710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 160; DB 3; I
29.0%; Pred. No. 2.1e-05;
iive 46; Mismatches 3;
                                                                                                                                                                                65.0%; Score 160; DB 3; ilarity 29.0%; Pred. No. 1.7e-05; Conservative 46; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203442110710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-881-037-63
; Sequence 63, Application US/08881037
; Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2(TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 813-5600 TELEFAX: (650) 494-0792
                                        LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 29.03
Matches 20; Conservative
  INFORMATION FOR SEQ ID NO:
                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                      Best_Local Similarity
Matches 20; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: Si
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                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                62 XXXXXXNR 70
                                                                                                    ; TOPOLOGY:
US-08-881-037-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/443,540 FILING DATE: 18-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 164; DB 3;
Pred. No. 9.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46; Mismatches
                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUTCATION INFORMATION:
TELEPHONE: (650) #33-5600
TELEPAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 755 Page Mill Road CITY: Palo Alto
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.7%;
Best Local Similarity 30.0%;
Matches 21; Conservative 40
FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 SAVYYCAKGR 100
                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 XXXXXXXNR 70
                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-881-037-62
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US-08-881-037-17
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ADDRESSEE:
STREET: 7
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                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Nalease #1.0, Version #1.30
FILLING DATE: 23-400-1997
                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Glick, Gary D.
APPLICANT: Samanson, Batrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STREET: GA
COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/ABENT INFORMATION:
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18-5600
TELECOMMUNICATION 18-5600
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                                                                                                                                                                                        Sequence 59, Application US/08881037
Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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Best Local Similarity
Matches 20; Conservi
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                                                                                          AVYYCAKGR 100
                                                      62 XXXXXXXNR 70
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US-08-881-037-59
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US-08-235-838-11
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Gaps
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                                                                  APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
SOFTWARE: PAETOTION DATA:
APPLICATION NUMBER: US/08/235,838
FLING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FLING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION NUMBER: 35,129
REFERENCE/DOCKET NUMBER: 31.029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 157.5; DB 1;
; Pred. No. 0.00031;
47; Mismatches 10;
                                                                                                                                                                                             E: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
                      Groner, Bernd
Hardman, No. 5571894man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-465-473B-11
Sequence 11, Application US/08465473B
Patent No. 5939531
GENERAL INFORMATION:
Harwerth, Ina-Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 SAVYYCAKG-GASGDWYFDV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.0%;
27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-235-838-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                USA
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63 SYWMWAYQRPGQGLEWIGMIDPSDSETQYNQMFKDKAALTVDKSSNTAYWQLSSLTSED 122
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APPLICANT: Groner, Bernd
APPLICANT: Archan, No. 5939531man
APPLICANT: Archan, No. 5939531man
APPLICANT: Zwickl, Markus
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for TITLE OF INVENTION: Growth Factor Receptor NUMBER OF SEQUENCES: 34
ADDRESSEE: ANDARIES COPRESS:
ADDRESSEE: 564 MORTIS Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAIL:
COUNTRY: USA
ZIP: 07901-6940

COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
JAPPLICATION DATA:
                                                                                                                                                     APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION NUMBER: US/08/235,838
FILING DATE: TBA
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-3AN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGERT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 16:
SCOURMER: (919)541-8619
INFORMATION FOR SEQ 1D NO: 16:
SCOURMER: GARACTERISTICS:
                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.0%; Score 157.5; DB Best Local Similarity 27.5%; Pred. No. 0.0058; Matches 22; Conservative 47; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08465473B Patent No. 5939531 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wels, Winfried S. APPLICANT: Hynes, Nancy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 SAVYYCAKG-GASGDWYFDV 141
   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 637 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-235-838-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-465-473B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08235838
Fatent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Are and a Applicant Groner, Bernd
APPLICANT: Zwick! Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION 1435
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PROR APPLICATION NUMBER: US 07/828,832
FILING DATE: 05-FEB-1991
APPCRATOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 05-FEB-1991
APPCRATOR APPLICATION NUMBER: US 091-810079.3
FILING DATE: US-FEB-1991
APPCRATION NUMBER: 22,640
REGISTRATION NUMBER: 22,640
REGISTRATION NUMBER: 22,640
REGISTRATION NUMBER: 22,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.0%; Score 157.5; DB 2; 27.5%; Pred. No. 0.00031; tive 47; Mismatches 10;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAVYYCAKG-GASGDWYFDV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 241 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 27.59
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                   ZIP: 07901-6940
COMPUTER READABLE FORM:
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                                                                                                   Summit
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-235-838-16
                                                                                                                                   STATE: N
COUNTRY:
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Gaps
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nilarity 27.1%; Pred. No. 4e-05;
Conservative 48; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION DATA:
APPLICATION DATA:
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540 FILING DATE: 18-MAY-1995
                                                                                                                                                                            Score 157; DB 3;
Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-881-037-60

Sequence 60, Application US/08881037

Patent No. 6080588

GENERALION:
APPLICANT: Gilck, Gary D.
APPLICANT: Swanson, Patrick C.
TILLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: MONTISON & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                    48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                         Query Match 63.8%;
Best Local Similarity 27.1%;
Matches 19; Conservative 4
                              LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
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amino acid
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            SEQUENCE CHARACTERISTICS:
                                                                    SS: single
linear
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Best Local Similarity
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ZIP: 94304-1018
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US-08-881-037-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.0%; Score 157.5; DB 2; 27.5%; Pred. No. 0.0058; tive 47; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION: 530
                                                                                                                                                                                             4-18518/A/CIP/CONT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31.-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY,AGENT INFORMATION:
NAME: Pfelfer, Hesna J.
REGISTRATION NUMBER: 22,640
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-WAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KONSK!, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344211071
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 SAVYYCAKG-GASGDWYFDV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 XXXXXXXXNRDYSNNWYFDV 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.59
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-473B-16
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31 SYWIHWVKQRPGQGLEWIGEIDPSDNYTYYNQKFKGKATLIVDKSSSTAYMQLSSLISED 90 QQ

61 XXXXXXXNR 70 :::::::| 91 SAVYYCAKGR 100 Oy Op

Search completed: August 14, 2002, 15:17:02 Job time: 685 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:07:32 ; Search time 108.64 Seconds (without alignments) 70.758 Million cell updates/sec Run on:

2\_G\_3\_G\_4
246
1 SYWMQXXXXXXXXXXXXXXXX

Scoring table:

Title: Perfect score: Sequence:

80

BLOSUM62DX Gapop 10.0 , Gapext 0.5

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	antibody	Iq heavy		מו	מ	מו	Ig heavy	Ig heavy	Ig heavy	ъ	ь		Ig heavy	ъ	б		ь	ь	Ig heavy	Б	ъ	Ig heavy	Б	ь	ь	ь	5	Б	Ig heavy
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SUMMARIES	ID	S53751	PH1160	S26463	PH1162	PH1161	PL0089	B22769	PL0086	S41394	PH1426	S25175	S20643	н37262	D25150	MHMS4E	T01407	C30560	PH1004	PH1005	MHMS15	MHMSJ5	HVMS02	S24287	S20646	PH1521	B30560	A27472	B47159	PH0987
	DB	~	~	7	7	7	7	7	7	~	7	7	7	7	~	-	~	7	7	7	-	Н	Н	~	7	~	~	7	7	N
	Query Match Length	116	86	111	87	88	119	120	119	120	122	120	122	101	69	117				106							123			107
di	Query	76.4	68.7	œ	67.1	vo.	9	65.2	65.0	64.8	9. 49	62.2	61.8	61.4	61.0	61.0	61.0	9.09	60.2	0.09	0.09	59.3	58.9	58.9	58.9	58.5	58.5	58.3	58.3	58.1
	Score	188	169	167.5	165	163	163	160.5	160	159.5	159	153	152	151	150	150	150	149	148	147.5	147.5	146	145	145	145	4	144	•	43.	4
	Result No.	1	7	e	4	S	9	7	œ ·	თ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Third heavy chain V region (clone 7A.1) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: No-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996
C.Accession: PH1160
R.Schittek, B.; Rajewsky, K.
A. Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A.Reference number: PH1105; MUID:92364545
A.Accession: PH1165
A.Accession: PH1166
A.Residues: 1-98 «SCH»
A.Residues: 1-98 «SCH»
A.Residues: 1-98 words: Immunoglobulin v region; immunoglobulin homology
C.Superfamily: immunoglobulin homology <IMM>
F:15-98/Domain: immunoglobulin homology <IMM>

68.7%; Score 169; DB 2; Length 98; 30.9%; Pred. No. 2e-05;

Query Match Best Local Similarity

30	143	58.1	118	77	A2	A24754		heavy	chain	> :	L 1	
32	141.5	57.5	101	v ~	L G			heavy		> >	- 14	
33	141	57.3	98	7	Ы			heavi		>	L	
34	140.5	57.1	137	~	PF			heavy		>	L.	
35	140	56.9	102	~	ď			heavy		> :	u	
36	140	56.9	114	7 (	<u>.</u>			heavy	chain	> >	<b>.</b> .	
38	140	, o	110	4 0		DH1517		heavy		> >		
9 6	140	56.9	119	4 (	2 4			neavy heavy		- >		
40	140	56.9	119	(7	E E			heavy		>		
41	140	56.9	119	~	PF			heavy		>	Su	
42	140	56.9	119	7	PF			heavy		>	L	
43	140	56.9	119	~	Z :	512		heavy	-	> :	L I	
44	140	56.9	138	N (7)	7 2		191	heavy	chain	> >		
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S53751	7											
antibody	antibody Fab Jel	1 103 he	103 heavy chain	air e	- 4	mouse						
C; Date:	23-Aug-	1995 #se	adneuce	, a	ev is	ion 19-Oct-1995 #text_change	ange		17-Mar-199	66		
C; Access R; Pokku]	sion: 55 luri, P.1	3/31 R.; Bout	hillie	Ĥ	Ŧ.	F.; Li, Y.; Kuderova, A.; Lee,	ee'	٦.,	Cygler,	Σ		
J. Mol.	Biol. 24	43, 283-	-297, 1	966			•		:			
A; Title: Preparation, characterization and A; Reference number: S53750; MUID:95018269	Title: Preparation, characterization and Reference number: \$53750; MUID:95018269	ation, c ber: S53	sharact 3750; M	eri	zat  ):95	i crystallization	oţ	an an	antibody	Fab	b tragm⊖n	den Len
A; Access	sion: S5	3751 niparu										
A; Molecu	ule type	: mRNA										
A; Residi C; Superi	A;Residues: 1-116 <pok> C;Superfamily: immunoglobulin V region;</pok>	16 <pok> immunogl</pok>	lobulin	>	reg	ion; immunoglobulin homology	,log	٠.				
F; 15-98,	15-98/Domain: immunoglobulin homology	1mmunoç	jlobuli j	 	JOH	ology <imm></imm>						
Query Best 1	atc cal	milarity	32	.98;		ore 188; DB 2; ed. No. 5.5e-07	11(	;	Ċ		ć	
Matches		Conser	conservative		: / ‡	Mismaccnes 4; inde	ST	ò	ซ		: <b>,</b>	
οy	1 SYWMQ3	XXXXXXX	XXXXXX	EI	PSI	SYMMOXXXXXXXXXXXXEIDPSDSYTNYNOKFRGXXXXXXXXXXXXXXXXXXXXXXX	CXXX	XXXX	09 XXX			
qq	31 SYWMON	WVKQRPGC	GLEWIG	H	PSE	SYMMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKGKATLTVDTSSSTAYMQLSSLTSED	VYMQI	SSLT	SED 90			
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Best Local Similarity
Matches 21; Conserv
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Matches 22; Conserv
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A; Residues: 1-119 <MEE>
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-88 <SCH>
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J. Exp. Med. 176, 427-438, 1992
A;Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A;Reference number: PH1105; MUID:92364545
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Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Datie: 06-Jan.1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (clone 10C.2A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1162
R;Schittek, B.; Rajewsky, K.
                                                      Gaps
     Gaps
                                   81
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A;Molecule type: mRNA
A;Residues: 1-11 < KAV>
A;Residues: 1-11 < KAV>
A;Cross-references: EMBL:X59113; NID:g51922; PIDN:CAA41839.1; PID:g51923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology < IMM>
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A; Residues: 1-87 <SCH>
A; Residues: 1-87 <SCH>
A; Experimental source: B cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 6-87/Domain: immunoglobulin homology <IMM>
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.1%; Score 165; DB 2; 31.8%; Pred. No. 3.7e-05;
 Mismatches
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                                                                                                                                                                                                                                                                                                        R.Kavaler, J. submitted to the EMBL Data Library, April 1991 A; Reference number: S26459 Accession: S26469
 47;
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Best Local Similarity
Matches 23; Conserv
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Matches 21; Conserv
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21;
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C;Accession: PL0089
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoul, M.; Urbain, J.; J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s A;Reference number: PL0080; MUID:89094248
A;Accession: PL0089
                                                                                                                                                                                           somatically mutated memory B cells in mice.
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A;Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal
A;Note: sequences from two other clones (18528-16 and 12584-3) were almost identical
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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                C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1161
S;Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A;Title: Natural occurrence and origin of somatically mutated memory B cells A;Reference number: PH1105; MUID:92364545
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C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region (12518-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                 A:Experimental source: B cell
C;Superfanily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;7-88/Domain: immunoglobulin homology <IMM>
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- mouse (fragment)
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Pred. No. 8.9e-05;
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chain V region (clone 13B.2A)
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64.8%;
29.1%;
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Best Local Similarity 29.1%
Matches 23; Conservative
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A; Experimental source: PBMC
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nes 19; Conserv
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A; Residues: 1-120 <MON>
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A; Molecule type: mRNA
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              A;Status: preliminary
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Best Local S:
Matches 19
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541394
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Dete: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: 841394
R;Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
Submitted to the EMBL Data Library, January 1994
A;Reference number: 541393
A;Accession: 841394
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                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                65.2%;
29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 23; Conserv
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nes 21; Conserv
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Best Local Si
Matches 21;
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R; van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A; Title: Molecular evolution of the human immunoglobulin E response: High incidence o
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A; Molecule type: mRNA
A; Residues: 1-120 <MAR>
A; Cross-references: BMBL:229586; NID:9452354; PIDN:CAA82703.1; PID:91334080
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibodies to
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X67620; NID:951856; PIDN:CAA47878.1; PID:9938260 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                 1 SYWMQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       31 SYWMHWYKQRPGQGLEWIGEIDPSDSYTYYNQKFKGKATLTVDKSSSTAYMQFSSLTSED 90
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s. Description: Structure and binding properties of monoclonal ant A; Reference number: $25174
A; Recession: $25175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (clone P2-57) - human (fragment)
                                                                                                                                                                                                                                                                   ; Score 159.5; DB 2;
; Pred. No. 0.00018;
47; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 159; DB 2;
Pred. No. 0.00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: the authors translated the codon AAA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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C; Keywords: heterotetramer; immunog.cbulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: PH1409; MUID: 93115676
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24.4%; Predictive 53;
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9 82

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C. Accession: A02039
B. Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
B. Biochemistry 21, 5415-5424, 1982
B. Reference number: A02039; MUID:83075344
A. Reference number: A02039; MUID:83075344
A. Accession: A02039
B. Reference number: A02039; MUID:83075344
A. Accession: A02039
B. Reference number: A02039; MUID:83075344
A. Accession: A02039
B. Reference number: A02039; MUID:83075344
C. Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context C. Comment: This protein binds dextran.
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: glycoprotein; heterotetramer: immunoglobulin
F. 15-96/Domain: immunoglobulin bromology < IMM>
F. 15-96/Domain: immunoglobulin bromology < IMM>
F. 12-96/Disulfide bonds: #status predicted
F. 15-Binding site: carbohydrate (Asn) (covalent) #status atypical
                                                                                                                                                                                                                                                                                             Ig heavy chain V region (AC38 260.2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 05-Unn-1887 #sequence_revision 05-Unn-1987 #text_change 16-Aug-1996
C; Accession: D25150
R; Didrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984
A;Title: A V region determinant (idiotope) expressed at high frequency in B lymphocyt
A;Reference number: A91000; MUID:84182519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SYMMNWIKQRPEQGLEWIGRIDPYDSETHFNQKFKDKAILTVDKSSSTAYMQLSSLTSED
        1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 SYWMHWVRQRPGQGLEWIGEIDPSDSYTNYNQKFKGRATLTVDKSSSATYM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-69 <DIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.0%; Score 150; DB 2;
41.2%; Pred. No. 0.00053;
:ive 29; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%; Score 150; DB 1;
25.3%; Pred. No. 0.0012;
Live 53; Mismatches 2.
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                                                                                                                61 XXXXXXXXNRDYSNNWY 77
                                                                                                                                                     83 SAVYYCARSYDYLPPWF 99
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Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C; Accession: $20643
R; Losman, M; Fasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A. Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A; Reference number: $20639
A; Reference number: $20639
A; Accession: $20643
A; Accession: $20643
A; Residues: 1-122 <LOS>
A; Residues: 1-122 <LOS>
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R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
B;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
A;Title: Common structural features among monoclonal antibodies binding the same antiger
A;Reference number: A38601; MUID:91115823
A;Accession: H37262
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C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                   Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                62.2%; Score 153; DB 2; L
26.8%; Pred. No. 0.00068;
ive 49; Mismatches 5;
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Pred. No. 0.00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                        91 SAVFYCAREKITDDYN---YFD 109
                                                                                                                                                                                                                                                                                                        61 XXXXXXXNR---DYSNNWYFD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 61.8%;
1 Similarity 25.4%;
18; Conservative 4
                                                                                Query Match 62.2%
Best Local Similarity 26.8%
Matches 22; Conservative
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Best Local Similarity 23.4%
Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserva
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A; Residues: 1-101 <GOS>
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Gaps

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Length 69; Indels 5

Length 117;

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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:11:47; Search time 53.64 Seconds (without alignments) 57.747 Million cell updates/sec

Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	P01756 mus musculu	snw.	POI/5/ MUS MUSCUIU	mus	mus	Snu	mus	Snu	POC320 mus musculu		3 mus	mus	SUM	mus	P01808 mus musculu	P01811 mus musculu	P01759 mus musculu	P01809 mus musculu	P01755 mus musculu	P23083 homo sapien	P23667 xenopus lae	P01743 homo sapien	_	P06327 mus musculu	P01807 mus musculu	P01793 mus musculu	P01741 mus musculu	P01787 mus musculu	)5 ratt	35 mus	P01806 mus musculu
DOMMARIES	HV12_MOUSE	HV50_MOUSE	HVI3_MOUSE	HV03 MOUSE	HV07_MOUSE	HV48_MOUSE	HV02_MOUSE	HV05_MOUSE	HVOI MOUSE	HV04 MOUSE	HV09 MOUSE	HV10_MOUSE	HV49_MOUSE	HV42_MOUSE	HV38_MOUSE	HV41_MOUSE	HV15_MOUSE	HV39_MOUSE	HV11_MOUSE	HV1G_HUMAN	CO3_XENLA	HV1B_HUMAN	HV40_MOUSE	HV52_MOUSE	HV37_MOUSE	HV24_MOUSE	HV00_MOUSE	HV18_MOUSE	HV01_RAT	HV26_MOUSE	HV36_MOUSE
Length DB	1		117 1																											144 1	
% Query Match L	61.0	60.0	, a	56.9	56.7	54.3	54.1	53.7	0.7.6	50.8	50.4	50.4	50.4	49.2		45.1	•	44.5	٠	•	44.1	•	•	42.7		42.5	42.3	٠		42.1	4.1.y
Score	150	147.5	145	140	139.5	133.5	133	132	125 5	125	124	124	124	121	113.5	111	110	109.5	109.5	109	108.5	108	107	105	105	104.5	104	103.5	103.5	103.5	103
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RESULT 2
HV50\_MOUSE
TO HV50\_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 12-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region AC38 15.3.

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P01789 P30193 P44764 P01791 P01791 P01791 P01792 P01663 P15436 P017436 P017436 P017436	Euteleo Murina Sibley Omology F THIS	tch al Similarity 25.3%; Pred. No. 0.00043; al Similarity 25.3%; Pred. No. 0.00043; 20; Conservative 53; Mismatches 2; Indels 4; Gramoxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
!	pdate) update; update; a; Verte nathi; N i E LIGHT DEXTRAI ARITY. (GLCNAC	0; DB 1; con 0.00043; tches 2 FKGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
HV20 MOUSE EPIZ_STAEP CN16_HAEIN HV19_MOUSE HV22_MOUSE HV23_MOUSE KRE6_CANAL API_SCHPO	TANDARD; PRT; 117 A  101, Created) 118, Last sequence update 119, Last annotation upda 110, Last annotation upda 1117  12, Last annotation upda 12, region MOPC 104E. 10a; Chordata; Craniata; Ve 10a; Chordata; Craniata; Ve 10a; Chordata; Craniata; Ve 10a; Chordata; Craniata; Ve 10a; Rodentia; Sciurognathi 11; PubMed-6816276; 11; Rodentia; Sciurognathi 11; The SEQUENCE OF THE LIG 12, THE SEQUENCE OF THE LIG 13, THE SEQUENCE OF THE LIG 14, THIS PROTEIN BINDS DEXT 154: THIS PROTEIN BINDS DEXT 160; 11 160; 11 160; 11 160; 11 17 183: THIS PROTEIN BINDS DEXT 160; 11 160; 11 160; 11 17 184: 11 185: NILINED (GLC 117 187: 11 188: 11	Score 150; D Pred. No. 0.0 3; Mismatches DSYTNYNQKFKCXX :  :      ::
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122 657 657 123 123 123 1097 147 652	SE STANDARD; PRT;  886 (Rel. 01, Created)  886 (Rel. 01, Last sequence  989 (Rel. 38, Last annotations of the chain V region MOPC 1046.  11us (Mouse).  11us (Mouse).  12us Metazoa; Chordata; Cranist Metazoa; Chordata; Cranist Metazoa; Chordata; Cranist Delibor; Etheria; Rodentia; Sciurring of the constant region domains stry 21:5415-5424(1982).  12us Also BEEN DETERMINE STRY 21:5415-5424(1982).  12us Also BEEN DETERMINE OF STRY 31:11 (1994).  12us Also BEEN DETERMINE OF STRY 31:11 (11) Also 113 Also 11	al Similarity 25.3%; 20; Conservative 53 20; WAGAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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                                                                                                          32 YYMKWVKQSHGKSLEWIGDINPNNGGTSYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CS7BL/6;
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                               Mús musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- MISCELLANGOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIT, A02012; HYWRO12.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003596; Ig_V.
Employed (194) 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.9%; Score 145; DB 1; Length 117; Best Local Similarity 26.5%; Pred. No. 0.0011; Matches 18; Conservative 46; Mismatches 4; Indels
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                    22.8%; Pred. No. 0.00094;
tive 54; Mismatches 3; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 102 precursor.
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(Rel. 38, Last annotation update)
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BY SIMILARITY.
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                    Best Local Similarity 22.8%
Matches 18; Conservative
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21-JUL-1986 (
15-JUL-1999 (
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P01747;
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P01750;
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HV03_MOUSE
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HV06_MOUSE
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                                                                                                                       A Didrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

A Didrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

T Vapion determinant (idiotope) expressed at high frequency in B serooded by a large set of antibody structural genes.";

I EMBO J. 3:517-523(1984).

R PIR; A02037; MHMS15.

R InterPro: IPR003596; Ig_V.

R Pran: PR00047; Jg; 1.

R SMART: SM00406; IGv; 1.

W Immunoglobulin V region.

T DOMAIN 99 105 D SEGMENT.

T DOMAIN 106 120 J SEGMENT.
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OF
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schilling J., Clevinger B., Davie J.M., Hood L.;
Schilling J., Clevinger B., Davie J.M., Hood L.;
Amino acid sequence of homogenecus antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).
-1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALS BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
-1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%; Score 147.5; DB 1; Length 120; 25.0%; Pred. No. 0.00073; tive 50; Mismatches 9; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                  13311 MW; 914453F426F09834 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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BY SIMILARITY.
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INTERPOS IPRO03006; IG_MHC.

INTERPOS IPRO03596; IG_V.

INTERPOS IPRO03596; IG_V.

SMART; SM00406; IGV: 1.

Immunoglobulin V region.
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Matches 20; Conservative
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PIR; A02034; MHMS18.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00407; 1g; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; S1gnal.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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                      EMBL; J00529; AAA38170.1; -.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                              The genetic basis of antibody production: the dominant anti-arsonate
                                                                                                                                                                                                               idiotype response of the strain A mouse.";

Eur. J. Immunol. 12:1029-1032(1982).

-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER

DIFFERENTATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
Ig heavy chain V region 36-65.
Mas musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia<u>:</u> Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 56.9%; Score 140; DB 1; Length 120; Best Local Similarity 20.3%; Pred. No. 0.0032; Matches 16; Conservative 53; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SW00406; IGV; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
NON TER
SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                     MEDLINE-83131846; Pubmed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 139 AA. P01751; PRT; 139 AA. P01751; P01752; P01752; P01752; P01752; P01751; P01752; P01751; P01752; P01751; P01752; P017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-81234548; PubMed-6788376;
                                                                                                                                                                                                                                                                                                                                 PIR; A02028; HVMSG7.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                              Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                    [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 SEGMENT, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                               NCBI_TaxID=10090;
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HV07_MOUSE
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Gaps
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Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Illegitimate recombination generates a class switch from C mu to C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                            IG HEAVY CHAIN V REGION B1-8/186-2.
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                                                                                                                                                                                                                                                                                                                                                           Length 139;
                                                                            COMPLEMENTARITY-DETERMINING-1.
                                                                                                                              COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-1.
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139 IG HEAVY CHAIN V REGION B1-6
49 COMPLEMENTALI.
54 COMPLEMENTALITY - DETERMINING
68 COMPLEMENTARITY - DETERMINING
117 FRAMEWORK - 3.
124 D SEGMENT.
139 JH2 SEGMENT.
115 BY SIMILARITY.
139
A; 15419 MW; 1B57DD4FDCC9F465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
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                                                                                                                                                                                                                                                                                                                                                         56.7%; Score 139.5; DB 1; 22.8%; Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR, A02033; HVWST7.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region TEPC 1017 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
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pfam; P00047; 19; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
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STANDARD;
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54
68
85
117
                                                                                  Mus musculus (Mouse)
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                        STRAIN-C57BL/6;
                                                                                                                                                                                                                 Baltimore D.;
HV05_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV01_MOUSE
P01745;
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DISULFID
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SEQUENCE
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DOMAIN
DOMAIN
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                                                                                                   50 SYGINWYKQRPGQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSED 109
                                                       Gaps
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                                                                                  SYWMQXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                         Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.1%; Score 133; DB 1; Length 140; 19.0%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 93G7
                                                    7; Indels
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                         54.3%; Score 133.5; DB 1;
18.2%; Pred. No. 0.015;
iive 55; Mismatches 7;
                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 havy chain V region 9367 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Mismatches
                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                     110 FAVYYCARSDGY-YDWF 125
                                                                                                                                         61 XXXXXXXXNRDYSNNWY 77
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Matches 15; Conservative
                                                      Conservative
                                                                                                                                                                                                                                            STANDARD;
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140 AA;
                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                         Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                          HV02_MOUSE
P01746;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
--- MISCELLANBOUGS THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA.
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                                                                                                                       Ig heavy chain V region 3 precursor.
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Baltimore D., "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 SYWMHWYRQRPGQGLEWIGNINPGRGTNINERFKSKYTLTVDKSSSTAYTQLSSLTSED 109
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                61
                                1 SYWMOXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXX 60
                2 YWWQXXXXXXXXXXXXXXXEIDPSDSYTNYNOKFKGXXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-6751BL/6;
MEDIINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12772 MW; C530F829C906F69B CRC64;
                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
heavy chain V region 23 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
HV09_MOUSE
HV09_MOUSE
STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 16-JUL-1999 (Rel. 38, Last annotation update)
DF 19-ABAY Châin V region 186-1 precursor.
OS Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK - 3
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MC.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                          92 AVYYCARGYGYDP---FDV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                         62 XXXXXXXNRDYSNNWYFDV
                                                                                                                                                                             STANDARD;
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20
50
55
69
86
11
117
117 AA;
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                                                                                                                                          Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes."; EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
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01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 205.12.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaeleostomi;
                                         MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDOBF CRC64;
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BY SIMILARITY.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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InterPro; IPR003596; Ig_v.
Pfam, PF00047; ig; 1.
SMART; SM00406; IGv: 1.
Immunoglobulin V region.
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Best Local Similarity 17.7%
Matches 14; Conservative
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Matches 16, Conservative
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118 AA;
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NCBI_TaxID=10090;
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                                                                                             "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 14:625-637(1981).
-1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:655-637(1981).

-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                            FRAMEWORK - 1.
COMPLEMENTARITY - DETERMINING - 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV:
Immunoglobulin V region; Signal.
                                                     STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
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                      NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musincel_TaxID=10090;
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"Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
Cell 40:271-281(1985).
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COMPLEMENTARITY-DETERMINING-2.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. BY SIMILARITY.	117 117 117 Aa; 12834 MW; B8862FAC67ABD345 CRC64;	Ouery Match Best Local Similarity 19.1%; Pred. No. 0.073; Matches 13; Conservative 4%; Mismatches 7; Indels 0; Gaps 0;	1 SYWWQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXXX 60      ::::::::::::          :    50 SYWMHWYKQRPGRGLEWIGNIDPNSGGTKYNEKFKSKATLIYDKPSSTAYMQLSSLTSED 109	
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein August 14, 2002, 15:10:52 ; Search time 187.61 Seconds (without alignments) 73.768 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table:

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562222 seqs, 172994929 residues Searched:

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SPTREMBL\_19:\* Database

1: sp\_archea:\*
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4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\* sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_rvirus:\*
sp\_bacteriap:\* sp\_organelle:\* sp\_phage:\* sp\_archeap:\* sp\_plant:\*
sp\_rodent:\* sp\_mhc:\* 12: 13: 14: 15: 16: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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# ALIGNMENTS

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STRAIN-C57BL/6;
KOZONO H., AZUMB T.;
KOZONO H., AZUMB T.;
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
Bydroxy-3-Nitrophenyl)Acetyl (NP).",
EMBL, AB069912; Bab63928.1; --
EMBL, AB069914; Bab63930.1; --
                                                                                                                                  Mus musculus (Mouse),
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                            091V67;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (V304-D-J-C MU PROTEIN) (FRAGMENT).
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              143 AA
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RESULT Q924P9

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51 YWMNWVKQRPGQGLEWIGAIDPPDSYTSYNQKFKGTTLTVDTSSSSAYMLLSSLTSEDSA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 SYWMOWYKQRPGGGPEWIGEIDPSDIYTDYNQEFKGKATLIYDTSSSTAYMQLSSLISED
                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.0 KDA PROTEIN.
HYPOTHETICAL 52.0 KDA PROTEIN.
EUKaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB067787; BAB63272.1;
SYWMQXXXXXXXXXXXXXXEIDPSDSSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; NUSI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.8%; Score 159.5; DB 11; Length 481; Best Local Similarity 27.3%; Pred. No. 0.029; Matches 21; Conservative 50; Mismatches 5; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013488; AAH13488.1; -. Hypothetical protein. SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-5-7-C MU PROTEIN (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.4%; Score 158.5; DB 11; 25.0%; Pred. No. 0.003; tive 48; Mismatches 11;
                                                                                                                                                                                                                         481 AA
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                                                                                                                                                                                                                         PRT;
                                                                                                                    SAVYYCAR-RYYGGODYW 107
                                                                                61 XXXXXXXXNRDYSNNWYF 78
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111 VYFCARGPRD-SSGYYW 126
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                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
Matches 20; Conserva
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SEQUENCE FROM N.A.
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SEQUENCE
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069916; BAB63932.1; -.
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP)."; Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB060910; BAB63926.1; -
                                                                                                                                                                                                                       Mus musculus (Mouse),
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;
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                                                                                            Q924P9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
V303-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.1%; Score 175; DB 11; 30.8%; Pred. No. 0.00014; tive 50; Mismatches 4;
                                                                                143 AA
                                                                              PRT;
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kozono Y., Kozono H., Azuma T.; "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                       Q9JL81;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                   114
12829 MW; 404885FDE6BA56F8 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%; Score 147.5; DB 11; 26.2%; Pred. No. 0.013; ive 49; Mismatches 9;
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                                                                                                                 114 AA
                                                                                                                                                                                                                                                                                         with cardiac myosin.;
Infect. Immun. 68:5803-5808(2000).
EMBL; AF206025, AAF69323.1;
HSSP, PO1810; 2FBJ.
InferPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_W.
Ffan; PF00047; ig; 1.
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                                                         SAVYYCARGL-YDGNWYFDV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAVYYCARSNYYGSSLYYFD 102
                                              80
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                                             61 XXXXXXXXNRDYSNNWYFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                PRELIMINARY;
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Best Local Similarity
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SEQUENCE
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Q924P5;
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Gaps
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB067795; BAB63280.1; -...
Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Babbl; AB069920; BAB63936.1; -.
NON TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinge; Musingel_TaxID=10090;
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_TaxID=10090;
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                                                                                                                                                                                                                                                                               DB 11; Length 144;
                                                                                                                                                                                                                                                                        59.3%; Score 146; DB 11; Length 1
24.7%; Pred. No. 0.028;
tive 49; Mismatches 8; Indels
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                                                                                                                                                                                  144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
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Best Local Similarity 23.8%
                                                                                                                                                                                                                                                                                                                                           20; Conservative
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                                                                                                                                                                                                                                                                                                               Best Local Similarity
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DB 11; Length 278;

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1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXX 60
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Kozono Y., Kozono H., Azuma T.;
Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067781; BAB63266.1;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                        Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -
SEQUENCE 278 AA; 29778 WW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16216 MW; 92460F1FDF1B7538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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22.5%; Pred. No. 0.3;
tive 51; Mismatches
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01-DEC-2001 (TIEMBLREL 19, Last seq
01-DEC-2001 (TIEMBLREL 19, Last ann
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                   110 SAVYYCTRGYGY-DDVYFDV 128
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                                                                                                                                                                                                                                                             Conservative
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146 AA;
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Matches 18; Conserv
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                                                                                           NCBI_TaxID-10090;
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Q924R8;
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SACORON Y., KOZONO H., AZUMA T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3 Nutrophenyl, Acetyl (NP).";

Submitted (AUG-2001) to HE EMBL/GenBank/DDBJ databases.

EMBL; AB069917; BAB63933.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V23.D-J-C MJ.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Euthelia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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9
                                                                                                                                                                                                                          58.1%; Score 143; DB 11; Length 117; llarity 21.8%; Pred. No. 0.032; Conservative 55; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.7%; Score 142; DB 11; Length 140; 22.8%; Pred. No. 0.055; tive 49; Mismatches 6; Indels
                          Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ22517; CAB65236.1;
HSSP; P01708; IMCP.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_w.
Ffam; PF00047; 1g; 1.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                  13060 MW; D816AD0858A47E4C CRC64;
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Last annotation update)
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0924P8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last ann
V23-D-J-C MU PROTEIN (FRAGMENT).
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01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                    117 1
117 AA;
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Rozono Y., Kozono H., Azuma T.;

**Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3 Nitrophenyl)Acetyl (MP).";

Submitted (AuG-2001) to PEBL/GenBank/DDBJ databases.

EMBL; AB067793; BAB63278.1;
                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.7%; Score 139.5; DB 11; Length 145; 22.8%; Pred. No. 0.094; Live 49; Mismatches 11; Indels 1;
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2001 (TrEMBLrel. 19, Last annotation update)
ANII-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 145
145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update) VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,11;
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Infect. Immun. 68:5803-5808(2000).
EMBL; Ar206029; AAF69327.1; ...
HSSP; PO1810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffan; PF00047; Iq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Matches 18; Conserv
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                                                                                                                                                NCBI_TaxID=10090;
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Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.1%; Score 135.5; DB 11; Length 143; 21.5%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB069915; BAB6391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;
                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Mismatches
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                                                                                                      PRT;
                                                                                                                                                                         V165-D-J-C MU PROTEIN (FRAGMENT).
V165-D-J-C MU.
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                83 SAVYYCARQRRNYAMDYW 100
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60 XXXXXXXXNRDYSNNWY 77
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                                                                                                                                                                                                                                                                                                                                                                                                               143
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Best Local Similarity
Matches 17; Conserv
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SEQUENCE FROM N.A.
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19: /SIDSI/gcgdata/hold-geneseqy-genebl/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseqy-genebl/AA1999.DAT:*
22: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2000
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Listing first 45 summaries
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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

14: 115: 117: 118: 22: 22:

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		dР			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	2517	100.0	470	21	AAW90933	Humanised anti-Fas
~	2515	99.6	470	21	AAW90934	Humanised anti-Fas
3	2514	6.66	470	19	AAW83037	Anti-Fas humanised
4	2514	99.9	470	21	AAB14779	Humanised anti-Fas
5	2514	99.9	470	21	AAW90929	Humanised HFE7A de
9	2514	6.66	470	21	AAW90935	Humanised anti-Fas
7	2501	99.4	470	19	AAW83036	Anti-Fas humanised
80	2501	99.4	470	21	AAB14776	Humanised anti-Fas
6	2501	99.4	470	21	AAW90926	Humanised HFE7A de
10	2495	99.1	470	21	AAW90936	Humanised HFE7A de
11	2346.5	93.2	731	22	AAM52156	Humanised HMFG-1 h

Humanised HWFG-1 h Humanised HWFG-1 h Humanised HWFG-1 h Heavy chain of hmA Heavy chain of hmA Humanised 313/A3 ( A dimeric anti-CD2 Chimeric anti-CD2 Chimeric anti-DD3 Chimeric anti-DD3 Gengence of antibo Human reshaped F19 Completely humanis Amino acid sequency AntiDody D heavy c Ganglioside GM2 an Human immune syste Recombinant immuno Humanised anti-IL- Humanised anti-IL- Chimeric mouse/hum Amino acid sequenc Anti-IL-8 humanise Anti-IL-8 humanise Anti-IL-8 humanise Anti-IL-8 humanise Human type antihum Human type antihum BDBIO heavy chain MOTADII fusion pro Human type antihum Reshaped CAMPATH-1	ALIGNMENTS  T. 1  AAM90933 standard; Protein; 470 AA.  AAM90933;  OB-AUG-2000 (first entry)  Humanised anti-Fas designed heavy chain Heu 1 protein.  Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-blergic; anti-arthritic; antidivial; immunoadulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-rheumatic; hepatotropic; anti-inflammatory; sylvenimetic; anti-rheumatical; appropriate; propriate; propria
AAM52159 AAM521516 AAM5215161 AAM52151 AAM52151 AAM482151 AAM48850 AAB08026 AAB08026 AAB08026 AAB08026 AAB08026 AAB08026 AAB08026 AAB08026 AAB08026 AAB080316 AAB080318 AAB080316	AA.  AA.  vy chain Heu  uy chain Heu  antiviral; is  ve; thyromin  neuroprotect  sis; systemi  ison's disea  ison's disea  ison's disea  ison's atteri  its; hepatit  tis; hepatit
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40000000040000000000000000000000000000	standard, Protein;  1 anti-Fas designed body; human; anti- rigic; anti-arthrit gical; immunosupr pic; humanized; ap syndrome; crohn selected; ap pic; pagendent diabetes pathy; glomerulone pic; pic; pic; pic; pic; pic; pic; pic;
WWW.021110000000000000000000000000000000	dard; (firs: (firs: i-Fas i-Fas i-hum i, ant. li im ant
	stand; ; 000 (; d antilibody; ergic; optic; optic; optic; scler; scler; scler; scler; scler; copathy copathy yege; 999;
2346.5 2341.5 2335.5 2335.5 2335.5 2230.5 2220.5 22	AAW90933 sta AAW90933 sta AAW90933; 08-AUG-2000 Humanised an trailergi mephrotropii hepatotropii
11111111110222222222222222222222222222	RESULT AAW90933 TD AAW6 XX
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This invention describes a novel numanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents completely and the normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidabetic, anti-allargic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antiviral, inflammatory dermatological, immunosuppressive, thyromimetic, antiviral, inflammatory of inflamed binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit in by competitive (disease associated with the Fas/Fas ligand system, especially systemic disease associated with the Fas/Fas ligand system, especially systemic disease, sjorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, soleroderma, Goodpasture syndrome, Confuse and disease, soleroderma, Goodpasture syndrome, confused and appearance of thibit apoptosis and promal calls but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu I symbol to the method of the invention.
                                                                                                                                                                                                                                                                                                                        infilamentsed anti-ras antibody, useful for treating or preventing e.g. infilamentory or autoimmune disease, induces apoptosis selectively in realist with sharement or a selectively in the sharement or a selective in the sharement of the selective in the sharement of the selective in the sharement of the selective in the selective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like
                                                            Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 169-170; 263pp; English.
                                                      Nakahara K,
                                                      Haruyama H,
                                                                                                                                                         WPI; 2000-258930/23.
                                                                                                                                                                                                                     N-PSDB; AAA11644
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470 AA; Sequence

ö WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240 420 61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 Gaps 9 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV ö 100.0%; Score 2517; DB 21; Length 470; 100.0%; Pred. No. 5.3e-143; Live 0; Mismatches 0; Indels 0; Query Match 100. Best Local Similarity 100. Matches 470; Conservative 301 181 301 361 g à 임 ò g οy g ŏ g à g å

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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting between
CC fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemnic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunoamodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiphosis by binding to cell surface Fas or inhibit it by competitive
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addisease, Siorgen's syndrome, sterility, mysathenta gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent dabetes mellitus, allergy, arterioscierosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatlitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
                                                                                                                                                                                                                                                                                                                                                                                                   Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosupressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodopasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating or preventing e.g. apoptosis selectively in
361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin dependent diabetes mellitus; arterioscierosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection
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                                                                       421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                           Humanised anti-Fas designed heavy chain Heu 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haruyama H, Nakahara K, Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2 ; Page 174-176; 263pp; English.
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                                                                                                                                                                                                               AAW90934 standard; Protein; 470
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                               (first entry)
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Location/Qualifiers

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inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; multiple solerosis; Basedow's disease;
                                                                                                                                                                   Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombopenia purpura; insulin-dependent diabetes; allergy; acppy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                 Indels
                                                                                                                                                              99.9%; Score 2515; DB 21;
99.8%; Pred. No. 7e-143;
11ve 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW83037 standard; Protein; 470 AA
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                                                                                                                                                                               Best Local Similarity 99.8
Matches 469; Conservative
                                                                                                                      470 AA;
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                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW83037;
                                                                                                                                                                 Query Match
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This is the amino acid sequence of the HV type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. It includes humanising R4dc and A7dr amino acid substitutions that are are conserved in the human igG heavy chain. Host Escherichia coli pyHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion fragment of the humanised HV type HFE7A heavy chain and DNA croding human igGl constant region (see AAV70080), and is deposited as FERM BP-6273 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of antibodies are used to evaluate, in onrmal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, soleroderma, Goodpasture syndrome, Crohn's disease, thromatopial arthritis, autoimmune haemolytic anaemia, Sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thromatopenia purpura and insulin-dependent diabetes), allentidies, atopy, arteriosclerosis, multiple scl rosis, Basedow's disease, thromatopenia purpura and insulin-dependent diabetes), allentidies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Page 225-227; 292pp; English.
                                              20..470
/label- Mat_protein
20..140
/label- Variable
                                /label- Sig_peptide
                                                                                                                 141..464
/label- Constant
                                                                                                                                                                                 /note= "claim 9"
69..84
                                                                                                                                                                                                                                          "claim 9"
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118..129
/label= CDR_H3
                                                                                                                                                     50..54
/label= CDR_H1
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97JP-0082953.
97JP-0169088.
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25-JUN-1997;
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 Key
Peptide
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Length 470;

Score 2514; DB 19; Pred. No. 8.1e-143;

99.98; 99.88;

Query Match Best Local Similarity

us-09-499-662-143.rag

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08-AUG-2000
                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Live or treating agent for the diseases caused by an abnormality Fas/Fas ligand system e.g. autoimmune diseases, contains \ensuremath{\mathsf{E}}
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                                                 GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                       MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                   WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                       LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                antibody; monoclonal antibody HFE7A; FERM-BP-5828;
Indels
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Mismatches
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Conservative
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469;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
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Pred. No. 8.1e-143;
1; Mismatches 0;
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1larity 99.8%;
Conservative
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Matches 469; Conserv
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This interior describes a nover numerized anti-ras antibody like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antidiabetic, antimifertility, neuroprotective, antiarteriosolerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cells unface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent inhibition of ligand binding. (1) are used to treat and/or prevent catsors associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, sjorgen's syndrome, pernicious or hypoplastic versus host disease, sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, rheumatoid arthritis, graft, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, and transplant rejection. (1) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine anti-body HERPA designed heavy chain which is used in the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
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Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel humanized anti-Fas antibody-like
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Pred. No. 8.1e-143;
1; Mismatches 0;
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                                                                                                                                                                                            05-APR-2000.
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                                                                                                                                                 EP990663-A2
                                                                                                           Synthetic
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anti-allergiz, anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; perphrotropic; antinfertility; neuroprotective; antiarteriosclarotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
                                                                                                     300
                                                                                                                                                                                                                             420
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240
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                                                           241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                   YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                             361 KAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                         470
                                                                                                                                                                                                                                                                                          421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                           Humanised anti-Fas designed heavy chain Heu 3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 180-182; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   AAW90935 standard; Protein; 470 AA.
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1998;
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appotosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematcosus; graft versus host disease; Sjogran syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatcoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin dependent diabetes; altergy; atteniosclerosis; myocarditis; cardiomyopathy; transplant rejection; therapy.

/label= Sig\_peptide 20..470 /label= Mat\_protein

/label= Variable /label- Constant

20..140

464

/note= "claim 9" /label- CDR\_H2 /note= "claim 9"

Region

50..54 /label= CDR\_H1

/label- CDR\_H3 /note- "claim 9

/label-

118..129

Region

Location/Qualifiers

Peptide Protein Region Region Region

Homo sapiens. Synthetic.

humanised antibody

Anti-Fas humanised antibody HFE7A heavy chain.

HFE7A; monoclonal antibody; mouse; Fas;

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care and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-anthitic, anti-inflammatory, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antiviral, cardiant and hepatropic activity. (I) induce antiarterioscierofic, cardiant and hepatropic activity. (I) induce cappetosis by binding to call surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent casease associated with the Fas/Fas ligand system, especially systemic upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Solorgen's syndrome, permitious or hypoplastic upus erythematosus, alsonedwis solorgened, permitions or hypoplastic disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-mas antibody heavy chain construct designated Heu 3 which is described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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Matches
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240 GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 61 ggglewmgeidpsdsytnyngkfkgkatltvdtststaymelsslrsedtavyycarnrd 120 121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMOWVKQAP 60 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 61 181 181 301 301 361 qq g g ò ò õ ద ò 유 ò g ò ò a

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This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. colipgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA encoding human igGl constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to evaluate drugs in animal models and to treat Fas-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 212-213; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases e.g. autoimmune disease,
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AAW83036 standard; Protein; 470

AAW83036 RESULT

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(first entry)

15-MAR-1999

SX EX

AAW83036;

New antibodies and proteins bind conserved epitope of Fas antigen

un O, Kimihisa I; Tohru T;

Jun O,

S, Shin Y,

Nobufusa Hidevuki H,

Masahiko O,

Akio S.

WPI; 1998-543440/47. N-PSDB; AAV70079

Hiroko Y,

97JP-0276064. 98AU-0059701

30-MAR-1998; 08-OCT-1997; 01-APR-1997; 25-JUN-1997;

AU9859701-A.

08-0CT-1998

97JP-0082953 97JP-0169088

(SANY ) SANKYO CO LTD.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                        treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus. Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AlDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                      MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                            241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                     301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                            361 KAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                    Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised anti-Fas antibody heavy chain, SEQ ID NO:89
                                                                                                                                    DB 19;
                                                                                                                                  Score 2501; DB 19;
Pred. No. 4.8e-142;
1; Mismatches 2;
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                                                                                                                                  99.4%;
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                                                                                                                                                       Conservative
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Chimeric - Homo sapiens.
                                                                                                                                              Similarity
                                                                                                     470 AA
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Best Local S:
Matches 467,
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The invention relates to compositions for the prevention or treatment containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the tracerdient or prevention of conditions such as autoimmune diseases, allery, acopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                                               for the diseases caused by an abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                                                                                                                                                                                                    in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
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; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2501;
                                                                                                                                                                                                                                                                                     Claim 21; Page 95-96; 139pp; Japanese.
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                                                                                                                                                                                    Preventive or treating agent
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98JP-0276883.
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                                                   (SANY ) SANKYO CO LTD
                                                                                                   WPI; 2000-485645/43.
N-PSDB; AAA72159.
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30-SEP-1998;
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Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic, antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized anti-Fas antibody, useful for treating or preventing e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakahara K, Tamaki I,
                                                                                                                                                                                           Humanised HFE7A designed heavy chain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells with abnormal Fas-Fas ligand systems
AAW90926 standard; Protein; 470 AA
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                                                                                                                                 (first entry)
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                                                                                                                              08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

computosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

anti-antenic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive thyromimetic,

antirheumatic, nephrotropic, antiinfertility, neuroprotective,

antirheumatic, nephrotropic, antiinfertility, neuroprotective,

contianteriosclerorlic, cardiant and hepatropic activity. (I) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

antirheumatics, neither fas/Fas ligand system, especially systemic

computosis by binding to cell surface Fas or inhibit it by competitive

inhibition of ligand binding. (I) are used to treat and/or prevent

computosis by binding to cell surface Fas or inhibit it by competitive

collessases associated with the Fas/Fas ligand system, especially systemic

cupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

collessase, autoimmune hemolytic anemia, sterility, myasthenia gravis,

conflictible sclerosis, Basedow's disease, thrombopenia purpura, insulin

collessase, autoimmune hemolytic anemia, sterility, myasthenia gravis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

colls. They bind to both human and murine Fas so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they minic

cells. They bind to both human and murine Fas so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they minic

che native ligand, do not induce liver disease, and have reduced risk of

inducing a human anti-murine antibody response. This sequence represents

a humanised anti-Fas antibody HEFAS as especials. Example reference 15; Page 134-136; 263pp; English.

470 AA; Seguence

(SANY ) SANKYO CO LTD.

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                                                                                                                                   GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                            241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                    361 kakgqprepqvytlppsreemtkngvsltclvkgfypsdiavewesngqpennykttppv 420
                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                          1 MGWSCIILFLVATATGVHSOVOLVOSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVS
                                                                                                                                                                                                                                                    WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                      YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                              KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
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   Length 470;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised HFE7A designed heavy chain HHH type protein.
Score 2501; DB 21;
Pred. No. 4.8e-142;
1; Mismatches 2;
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 99.48;
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98JP-0276882.
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                              Conservative
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999;
                Best Local Simi
Matches 467;
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   Query Match
Best Local 3
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361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

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into interaction describes a nover inumnized anti-ras antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an operation building binding between geotosis in cells with a normal system, by inhibiting binding between fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomoulatory, dermanciogical, immunosuppressive, thyronimetic, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce antiarteriosclerotic, cardiant and hepatropic activity. (1) induce inhibition of ligand binding. (1) are used to treat and/or prevent thinbition of ligand binding. (1) are used to treat and/or prevent systems associated with the Fas/Fas ligand system, especially systemic ulpus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, atteriosclerosis, myocarditis, cardiomypathy, glomerulonephitis, hepatitis (fulminant, chonic, viral (8), C or D) or alcoholic), and transplant rejection. (1) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic multiple a human anti-murine antibody response, This sequence represents inducing a human anti-murine antibody Hepsh heavy chain construct HHH type.
                                                                                                                        New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                         This invention describes a novel humanized anti-Fas antibody-like
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                        Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                        Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
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Pred. No. 1.1e-141;
                                                                                                                                                  inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                        Nakahara K,
                                                                                                                                                                                                            Claim 2; Page 188-189; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.18;
98.78;
                        Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464; Conservative
                                                              WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 AA;
                                                                                    N-PSDB; AAA11655
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                        Serizawa
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731 AA;
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Matches
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                                                                                                                     121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                        KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                    KAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                                                                    WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                  YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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121 181 181 241

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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytoctoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                         Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 gkglewvgeilpgsnnsrynekfkgrvtvtrdtstntaymelsslrsedtavyycarsyd 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSNNWYFDVWGOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound used to treat cancer has target cell-specific por comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Length 731;
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Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2346.5; DB 22
Pred. No. 1.4e-132;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Figure 7; 176pp; English.
                                                                                                      AA.
                                                                                                    AAM52156 standard; Protein; 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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02-OCT-2000; 2000US-237159P.
                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2001; 2001WO-GB01324
                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endonucleolytic activity
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                                                                                                                                                                                                                                                                                                              WO200174905-A1.
                                                                                                                                                               05-FEB-2002
                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                    Synthetic
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121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
             WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                         YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                              358 kakgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppv
                                                                                                                                                                                                                                                                                        KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPPV
                                                                                                                                                                                                                                                                                                  421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-662969/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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02-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                           polymorphic epithelial mucin; PEM1; I; human; cytostatic; cancer; apoptosis.
                                  300
297
                                                                              301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                        357
                                                                                                                               420
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                                               KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                              KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound used to treat cancer has target cell-specific por comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having
                                                                                                                                                                            LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                        Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
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                                                                                                                                                                                                                                                               Protein; 741
                                                                                                                                                                                                                                                                                                                                                           Humanised monoclonal antibody; cytotoxic; endonuclease; DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
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                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ANTI-) ANTISOMA RES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endonucleolytic activity
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                                                                                                                                                                                                                                                              AAM52159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                             05-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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         178
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Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                     portion
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                                                                        Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
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standard; Protein;
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22; Length 741;

93.2%; Score 2346.5; DB 22; Lengt 93.0%; Pred. No. 1.4e-132; .ive 20; Mismatches 10; Indels

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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM$21184 AAM$21184 and encoded by ABA02582-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis
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Pred. No. 2.7e-132;
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02-OCT-2000;
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                                                                                                    comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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92.9%; Pred. No. 6.3e-132;
iive 20; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES:
CORRESPONDEME ADDRESS:
ADDRESSEE: William M. Smith
                                                                                                                                                                                                                      ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Farcisco
STATE: California
                                                                                                                                                                                                                                                                                                                            ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.7%; Score 2232; DB 1; 93.1%; Pred. No. 2.8e-158; ive 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 03-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,23
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-326-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 449 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.1
Matches 420; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13
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5

8, A 45, 18,

US-08-466-163B-8 US-07-916-098A-45

Sequence

2116 2116 2116 2116 2116 2105 2105 2105 2105

US-09-109-207C-14 US-09-109-207C-16

-08-887-352B-18

US-09-296-005-14 US-09-296-005-16 US-08-487-550-8

Sequence Sequence Sequence

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us-09-499-662-143.rai

protein

MOLECULE TYPE:

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61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNR- 119
                                                                                                                                                                                                                                                     121 RQANFDRARVGWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                                                        EVKFNWYVDGVEVHNAKTKPREEOYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAP 354
                                                                                                                    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                         DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                        EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLXSVVTVPSSSLGTQTY1CNVNHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 IEKTISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 KITPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                     ;
6
                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
                                                                                     Indels
                                                                  Pred. No. 4.3e-158;
                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                     21; Mismatches
                                                    Score 2230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMM
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                  88.6%;
88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                   Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                    Query Match
Best Local Similarity
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US-08-378-939-10
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80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGTLVTV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.4%; Score 2200.5; DB 3 90.0%; Pred. No. 6.2e-156; iive 27; Mismatches 17;
                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genetech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/027,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                  CLASSIFCATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS:
   South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 90.09
Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          650/952-9881
                                             ZIP: 94080
COMEUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc.
                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
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US-09-026-985-71
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                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 186
                                                                                                                                                                                                                                                                                                                                                                                                                           7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEW 66
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Aresta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                Length 467;
                                                                                                                                                                                                                                                                                                                                                                            28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                              ; Score 2202.5; DB 4;
; Pred. No. 4.6e-156;
19; Mismatches 28;
                                                            39,132
R: PF-0497 US
                                        NAME: CETTONE, MIChael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                             87.5%;
89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Genentech, Inc.
1 DNA Way
                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                        Matches 414; Conservative
                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                              ; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                       TELEX:
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Length 452;

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421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-485-737B-67
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Pate
SEQ ID NO 67
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEG 300
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                                                           APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 87.4%; Score 2200.5; DB 4; Best Local Similarity 90.0%; Pred. No. 6.2e-156; Matches 407; Conservative 27; Mismatches 17;
                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Generator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                         NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genetech)
CURREWA APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILLING DATE: 20-Feb-1998
Sequence 71, Application US/09026985 Patent No. 6133426
                                              Gonzalez, Tania R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
                                                                                                                                                       ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2
CLASSIFICATION:
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APPLICANT: BUYSE, Marie-Ange
APPLICANT: BUYSE, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERPERON gamma-BINDING MOLECULES FOR TREATING SEPTIC.SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REPERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 1998-06-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
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86.5%; Score 2177; DB 4;
Best Local Similarity 88.2%; Pred. No. 3.6e-154;
Matches 410; Conservative 20; Mismatches 31;
US-09-485-737B-67; Sequence 67, Application US/09485737B; Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                              California
                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-934-373C-22
                                                               COUNTRY:
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        GENERAL INFORMATION:

APPLICANT: Buyes, Marie-Ange
APPLICANT: Buyes, Marie-Ange
APPLICANT: Buyes, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS.015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT APPLICATION NUMBER: PCT/EP 98/05165
FRIOR FILING DATE: 1998-08-14
FRIOR FILING DATE: 1998-06-18
FRIOR FILING DATE: 1998-06-18
FRIOR APPLICATION NUMBER: EPO 98870139.7
FRIOR APPLICATION NUMBER: EPO 97870122.5
FRIOR APPLICATION NUMBER: EPO 97870122.5
FRIOR FILING DATE: 1997-08-18
SOFTWARE: PALENT VERSION 3.0
SEQ ID NO 90
SEQ ID NO 90
SEQ ID NO 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            86.5%; Score 2177; DB 4; Length 711;
88.2%; Pred. No. 6.3e-154;
Live 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
PAPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: SYNTHETICUS-09-485-737B-90
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 88.2%
Matches 410; Conservative
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LLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 2161.5; DB 2;
; Pred. No. 4.9e-153;
17; Mismatches 28;
                     E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION BATA:

APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: Q7/715272
                                                                                     WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                       NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P070'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-1994
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.9%;
Best Local Similarity 89.4%;
                                                                                                                                                                                                                                                                                           FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 406; Conservative
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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80 NOKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136
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                                                                                                                                                    SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                  EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application PC/TUS9307832
Sequence 22, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                   437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                         421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUBBER: 07/715272
FILING DATE: 14-JUN 1991
PRIOR APPLICATION DATA: CTUGO APPLICATION NUBBER: PCT/US92/05126
FILING DATE: 15-JUN 1992
PRIOR APPLICATION DATA: CT/034373
FILING APPLICATION NUBBER: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 709P2PCT REFERENCE/DOCKET NUMBER: 709P2PCT FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
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INFORMATION FOR SEQ ID NO: 22:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
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                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPAtible OPERATING SYTEM: PC-DOS/MS-DOS SOFFWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/437,642B FLLING DATE: 099-May-1995 CLASSIFICATION: 530
                                   Sequence 22, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
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APPLICATION NUMBER: 07/934373
FILING DATE: 21.Aug-1992
PRIOR APPLICATION NUMBER: 08/146206
FILING DATE: 17.NOV-1993
PRIOR APPLICATION NUMBER: 08/146206
FILING DATE: 17.NOV-1993
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15.JUN-1992
PRIOR APPLICATION NUMBER: 07/715272
PRIOR APPLICATION NUMBER: 07/715272
FILING DATE: 14.JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, WendY M.
REGISTRATION NUMBER: 07/71020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P0709P2C1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-1994
TELEFAX: 650/25-981
INFORMATION FOR SEO ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 anino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
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Matches 406; Conservative
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US-08-437-642B-22
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                   US-08-437-642B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EDELMAN, LENA
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZORRK, MICHEL
APPLICANT: CHAABHII, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHMAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSFIEDR: 536
PRIOR APPLICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 94/10566
FILLING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                              437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08793450 Patent No. 6312690 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 8;
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TELEFAX: 7
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Sequence 14, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                                      120 Y--KWKYHGDWFDPWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 177
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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                121 YSNNW----YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
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Length 472;
85.2%; Score 2144; DB 4; Length 4
84.8%; Pred. No. 1e-151;
ive 27; Mismatches 37; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P1123
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
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TELEPHONE: 650/225-1489
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
Query Match
Best Local Similarity 84.88
Matches 403; Conservative
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INFORMATION FOR SEQ ID NO:
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US-08-887-352B-14
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FELECOMMUNICATION INFORMATION:
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
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                                                                                                                               Gaps
                                                                                                                                                         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                           259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                   Length 451
                                                                                                                              30;
                                                                                                 84.4%; Score 2124; DB 2; 87.6%; Pred. No. 3e-150;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-J01-1997
                                                                                                                              24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, Cra1g G.
RGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91,1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
COUNTRY: USA
             LENGIH: 451 amino acids TYPE: Amino Acid
                                                                                                                               Conservative
SEQUENCE CHARACTERISTICS
                                          Linear
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                        ; TOPOLOGY:
US-08-887-352B-14
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                                                                                                 Query Match
Best Local Simi
Matches 396;
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79 YNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFLYSKLTVDKS 438
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                              20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                                                                                                                                                      SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                          Length 451;
                                                                                                                                                                                                             84.4%; Score 2124; DB 2;
87.6%; Pred. No. 3e-150;
tive 24; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CANRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/08466151 Patent No. 6037453 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WinPatin (Genentech)
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                 LENGTH: 451 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                Best Local Similarity 87.6
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-E
SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                         ; TOPOLOGY: Linear
US-08-887-3528-16
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Gaps

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SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
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                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-109-207C-14
                                                                                                                                                                                                                                                      84.4%; Score 2124; DB 4; Length 4
87.6%; Pred. No. 3e-150;
Niematches 30; Indels
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1990-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RWOOGNVFSCSVMHEALHNHYTOKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                  Matches 396; Conservative
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                         FEATURE:
NAME/KEY: Artificial
                                                                                                                              TYPE: PRT ORGANISM: Artificial
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Job time: 688 sec
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Best Local S
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Improved Anti-1gE Antibodies and Method of Improving Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.4%; Score 2124; DB 3
87.6%; Pred. No. 3e-150;
tive 24; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                  P0718P2C1D1
PRIOR APPLICATION NUMBER: 08/466150.

APPLICATION NUMBER: 08/40517
FILING DATE: 06/40517
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
APPLICATION NUMBER: 08/185899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-109-207C-14

Sequence 14, Application US/09109207C
Patent No. 617213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
TITLE OF INVENTION: Improved Anti-IC
                                                                                                                                                                                    APPLICATION NUMBER: 07/744768 FILING DATE: 14-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                      APPLICATION NUMBER: 07/879495
                                                                                                                                                                                                                               NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SECTIONO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                                                                                                                                      FILING DATE: 07-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                               650/952-9881
                                                                                                                         PRIOR APPLICATION DATA:
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Matches 396; Conserva
                                                                                                                                                                                                                                                                                                                                                                            Amino Acid
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US-08-466-151-65
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

August 14, 2002, 15:18:59 ; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

US-09-499-662-143
2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score: Sequence:

283138 seqs, 96089334 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Iq qamma-1 chain C		gamma-3		gamma	gamma-4				Ig heavy chain pre	gamma		noclona	Ig gamma 2a chain			gamma chain C						gamma-3 heavy	gamma-1	gamma-3 chain				
	ID	СННО	A23511	A60764	537483	G2HU	G4HU	G2MS11	S40295	S01321	S22080	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	GIMS	PS0018	GIMSM	G3MSM
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% Query	Match	69.8	65.1	65.1	64.1	64.0				59.8	28.6			26.7	50.3	50.1	49.8	49.5			48.9		46.3	٠	45.9	•	45.5	•	45.3	45.3
	Score	1758	1639.5	1637.5	1613.5	1610	1599.5	1549	1547	1504.5	1474	1467	1432	1426.5	1267	1261	1253	1245	1235	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	4	14	1139
Result	 Q	Т	7	e	4	S	9	7	ထ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

330 1 G2MSA 329 2 C00847 339 1 G2MSAB 339 1 G2MSAB 322 2 S06611 405 1 G2MSBB 405 1 G2MSBB 547 2 147162 547 2 147162 549 2 S04845 549 2 S09131 246 2 S38950 240 2 A4944 572 2 B46529		Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	onc	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
120022222222222222222222222222222222222	G2MSA	S00847	G2MSAB	G2MSAM	PS0019	S06611	G2MSBM	147162	S38864	S14683	S04845	S69131	S38950	A49444	S69340	B46529
	0 1	5	5	9	2	7 2	5 1	7 2	89	7 2	5	1 2	9	2	7	2
	44.9	44.8	44.8	44.7	44.3	43.4	42.9	42.5	39.6	37.5	36.8	34.5	33.9	31.7	30.3	30.5
4444444444666 44444467966 9.0000000000000000000000000000000000	1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	966	943	925.5	867.5	854	798	762.5	759.5
1129 1127.5 44.8 1126.5 44.8 1114 44.7 1115 1093.5 1000 42.9 1070 42.0 1070 42.0 1070 42.0 1070 42.0 1070 42.0 1070 42.0 1070 42.0 42.0 42.0 42 42 42 50 50 50 50 50 50 50 50 50 50 50 50 50	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man) C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C.Accession: A93433, S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A93433; MUID:82274238
A; Accession: Add 434
A; Residues: 1-330 < ELL>
A.Cross.references: EMBE.221370 A.Gross.references bulle.221370 A.Gross.references bullet.2370
Lys-330 is removed after translation
R; Harris, L.J.
Submitted to the EMBL Data Library, October 1992 A.Reference number: 633904
A; Accession: S3861
A Molecule type: DNA
A. Krestudes: 2-30 kmm. A. Krestades: EMRH: 27770
R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A)TILLE: STRUCTURE Of human immunoglobulin gamma genes: implications for evolution of a peference number: 633887. MITH.83001043
A; Accession: S3887
A; Molecule type: DNA
A; Residues: 88-113; 235-330 <tpak></tpak>
A).Closs Teleflices: EMBL:L1/3/V R:Cunningham, B.A.: Rutishauser, U.: Gall, W.E.: Gottlieb, P.D.: Waxdal, M.J.: Edelma
11100
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A;Kelefatica number: A90.09; Mollo:/lloatuz4 A:Contents: mveloma protein Ru
A; Accession: B90563
A; Molecule type: protein
A; Kesiques; 1-90, 'K', '98-1-15> (CUN> a.Note: this seminance has the Clm/3) marker 07-ard
R;Rutishauser, U; Cunningham, B.A; Bennett, C; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Refrence number: A9U564; MUID:/IU64U25
A; Accession: A90564
A; Molecule type: protein
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R. Porstingl, H.; Hlschmann, N.
noppe 2941et s. 1 Mystor. Chem. 397, 1311004, 1370 A/Title: Die Primaerstruktur eines monoklonalen Iggl.Immunglobulins (Myelomprotein Ni

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c5, u) with an IGHG4 conv
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A; Residues: 1-377 <HUC>
A; Cross-references: GB:X03604; GB:M1295B; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics: GB:IGHG3
A; Genetics: GB:IGHG3
A; Genetics: GB:II9339; OMIM:147120
A; Map position: 14932.33-14932.33
A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                         R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                 Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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C.Species: Homo sapiens (man)
C.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Accession: A60764
R.Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A.Title: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an A.Reference number: A60764; MUID:90007613
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Rotherts: 2. Physiol. Chem. 364, 713-747, 1988
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A; Reference number: A91723; MUID: 83289131
A; Contents: myeloma protein KOL; disulfide bonds
A; Rocession: A91723
A; Mote: Lis sequence has the G1m(3) and G1m(non-1) markers
A; Note: this sequence has the G1m(3) and G1m(non-1) markers
B; Call, W.E.; Edelman, G.M.
B; Cochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565; MUID: 71064027
A; Contents: annotation; disulfide bonds
B; Cortents: annotation; disulfide bridges.
A; Contents: annotation; disulfide bonds
A; Reference number: A91667; MUID: 77070267
A; Consents: annotation; disulfide bonds
A; Contents: annotation; disulfide bonds
A; Contents: annotation; disulfide bonds
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A: Map position: 14q32.33-14q32.33
A: Map position: 14q41; 224/1
C: Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C: Superfamily: immunoglobulin hemology immunoglobulin hemology cimis immunoglobulin homology cimis
F: 120-85/Domain: immunoglobulin homology cimis
F: 127-306/Domain: immunoglobulin homology cimis
F: 127-31, 144-204, 250-308/Disulfide bonds: #status experimental
F: 103/Disulfide bonds: interchain (to heavy chain) #status experimental
F: 109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F: 100-Minding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 3.6e-93;
3; Mismatches 0;
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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
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99.1%;
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Ig gamma-2a chain - mouse
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Accession: 837483
R; Ducancel, F.F.D.
Submitted to the EMBL Data Library, February 1993
A; Reference number: 837483
A; Reference number: 837483
A; Accession: 837483
A; Status: preliminary
A; Molecule type: mRnA
A; Residues: 1-469 < DUC>
A; Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 276-345/Domain: immunoglobulin homology < LMM>
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                                                              Length 377;
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                                                                                                                                                                                         201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV----
                                                             Score 1637.5; DE
Pred. No. 3e-86;
7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.1%; Score 1613.5; Di
64.6%; Pred. No. 9e-85;
ive 59; Mismatches 10
                  ^IMB
C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology
                                                             Query Match 65.1%;
Best Local Similarity 82.8%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALHNHYTQKSLSLSPGK 470
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305; Conserv
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Best Local S
Matches 305;
                                                              Query Match
Best Local
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A; Residues: 1-326 CELL>
A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Note: Lys-326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an A; Reference number: A92809; MUID:81007873
A; Contents: myeloma protein Til
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and 264-268
60-Ala and in the amid
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A; Note: Trp-156 is at or near the complement-binding site
A; Note: Trp-156 is at or near the complement-binding site
A; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
A; Title: The mainto acid sequences of the three heavy chain constant region domains of
A; Reference number: A90752; MUID: 80001357
A; Contents: myeloma protein Zie
A; Accession: A90752
A; Molecule type: protein
A; Residues: 1-24, E', 26-57, EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q',
A; Note: this sequence has since been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma-2 chain C region - human C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Nati. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy of A;Reference number: A93906; MUID:82197621
A;Accession: A93906
                                                                                                                                                                                                                                                                                                                                                                                              417
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A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A:Reference number: A90253; WIDD:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                         NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                        359 ISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                  A, Contents: Zie
A; Accession: A93132
A; Molecule type: protein
A; Residues: 238-275 < HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revisions to residues 25, 59, 60, 8
A; Note: the revised sequence differs from that shown in having (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
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MOL. Influndol. 16, 923-925, 1979
A.Title: A note on the amino acid sequence
A;Reference number: A93132; MUID:80114419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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Query Match
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A. Map position: 14q32.33-14q32.33

A. Map position: 14q32.33-14q32.33-14q32

C. Superfamily: immunoglobulin C region; immunoglobulin homology

C. Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F. 20-85, Domain: immunoglobulin homology < IM2>

F. 239-306, Domain: immunoglobulin homology < IM2>

F. 239-306, Domain: immunoglobulin homology < IM2>

F. 239-306, Domain: immunoglobulin homology < IM3>

F. 239-306, Domain: immunoglobulin homology < IM3>

F. 27-83, 14d-200.246-304/Disulfide bonds: #status experimental

F. 27-83, 14d-200.246-304/Disulfide bonds: #status experimental

F. 102, 103, 106, 109, Disulfide bonds: interchain (to heavy chain) #status experimental

F. 176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C.Date: 02-Apr-1983 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C.Date: 02-Apr-1983 #sequence 16-Jul-1999
R.Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A.Fitle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A.Feference number: A90933; MUID:83157104
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A; Molecule type: DNA
A; Residues: 1-327 < ELL>
A; Molecule type: DNA
A; Residues: 1-327 < ELL>
A; Mote: the sequence was determined from the germline gene
B; Pink, J. R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Blacchem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid seque
A; Reference number: A90249; MuID:70207560
A; Accession: A90249
A; Accession: A90249
A; Accession: A90249
A; Residues: 1-30; 81-326 <PIN>
C; Genetics: C; Genetics: C; Apple A; Ap
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91.8%; Pred. No. 9.4e-85;
           G.
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           of immunoglobulin
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                                             A;Reference number: A93157; MUID:69064124
A;Contents: annotation; Sa, disulfide bonds
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A; Title: Structural studies A; Reference number: A93157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 303; Conserv
                                                                                                                                                         A; Gene: GDB: IGHG2
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A;Gene: GDB
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A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14932.33-14932.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (cComplex: An immunoglobulin heterotetramer subunit consists of two identical light (cComplex: An immunoglobulin heterotetramer; immunoglobulin cregion; learner; immunoglobulin pomology (c); Superfamily: immunoglobulin homology (c); Meywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IM3>
F;20-85/Domain: immunoglobulin homology <IM3>
F;34-203/Domain: immunoglobulin homology <IM3>
F;34-203/Domain: immunoglobulin homology <IM3>
F;34-307/Domain: immunoglobulin (colaban) #status experimental
F;37-83,141-201,247-305/Disulfide bonds: #status predicted
F;37/Kinding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Idgamma-2b chain - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C.Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C.Date: 31-Mar-1980 #sequence_revision 05 #2623; A26233; A53598
C.Stocession: 825057, A02157; A26235, A26233; A26233; A53598
R.Fischer, R.; Voss, A.; Niersbach M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the RMBL Data Library, July 1992
A.Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifile. A.Recession: 825057
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A;Nolecule type: mRNA
A;Residues: 1-474 <FIS>
A;Concers = 1.474 <FIS>
A;Concers = 1.474 <FIS>
A;Cosssion: 1.474 <FIS>
A;Cosssion: MID:g54826; PIDN:CAA47649.1; PID:g54827
A;Cosssion: A02157; MUD:g54826; PIDN:CAA47649.1; PID:g54827
B;Yamawaki: Fataoka, Y; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Pitle: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned frc
A;Reference number: A02157; MUD:80120716
A;Contents: a allele
A;Accession: A02157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSYFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%; Score 1599.5; DB 1; ilarity 91.8%; Pred. No. 3.7e-84; Conservative 9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germl:
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattl Science 206, 1299-1303, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
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C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C. Accession: $40.295 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C. Accession: $40.295 #seference number: $40.295 #steference number: $40.295 #second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin C region; immunoglobulin pyroglutamic acid
C; Superfamily: immunoglobulin C region (Fil-446/Product: Ig gamma-2a chain #status experimental cMAT>
F; 1-146/Product: Ig gamma-2a chain #status experimental cMAT>
F; 118-446/Domain: C region (CHT>
F; 118-446/Domain: C1 region (CH1>
F; 215-230/Region: hinge
F; 231-340/Domain: C2 region (CH2>
F; 341-446/Domain: C3 region (CH2>
F; 341-446/Domain: Immunoglobulin homology <IMM>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F; 22-96, 144-199, 2561-321, 367-425/Disulfide bonds: interchain (to lain) #status predicted
F; 224, 227, 229/Pisulfide bonds: interchain #status predicted
F; 224, 227, 229/Pisulfide bonds: interchain #status experimental
F; 224, 227, 229, Pisulfide bonds: interchain #status experimental
PIEKTISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                        SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNL
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Pred. No. 5.1e-81;
8; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Sco
64.6%; Pre-
tive 58;
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Best Local Similarity
Matches 292; Conserv
                                    298
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                                        A ARREFERENCE NUMBER: AZ5335, MUID: 80081501
A ACORDENTS: WEC 13
A ACCORDENTS: WEC 13
A MACOLECULE TYPE: MRC 14
A: RESENTOR AZ535
A: RACE C. 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-1306, 1303-130
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untranslated regions of the murine gamma2b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 KSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similaria,
Matches 293; Conservative
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross : 1-470 < SANA
A; Cross references: EMBL: X62916; NID: 9439; PIDN: CAA44699.1; PID: 9440
B; Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and a; Reference number: S06610; MUID: 90097956
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S31459
R;Patri, S.; Nau, F.
S; Nau, F.
S; Nau, F.
A;Reference number: S31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNR--D 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTP
                                                                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Residues: 142-470 <SYM>
A.Cross-references: EMBL:X16701
A.Note: the sequence was determined from the germline gene
C.Genetics:
A.Gene: 1g CH gamma-1
A.Introns: 98/1: 111/1; 221/1
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: 91ycoprotehn; heterotetramer; immunoglobulin; membrane p
F:161-225/Domain: immunoglobulin homology <IMM'
F:161-225/Domain: immunoglobulin homology <IMM'
F:181-225/Domain: ammunoglobulin homology cirky.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.6%; Score 1474; DB 2; Best Local Similarity 60.2%; Pred. No. 7.8e-77; Matches 284; Conservative 63; Mismatches 115;
            R;Sanders, P.G. submitted to the EMBL Data Library, November 1991 A;Reference number: $22080 A;Accession: $22080
C; Accession: S22080; S06610; A31303
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                                                                                                                                                                                                                                                                    C'Species: Mus musculus (house mouse)
C.bate: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Bloochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: S01320; MUID:88329081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GQGLEWIGEIYPGSGNSYFNEKFKGKATLIVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 KSCDKT-HTCPP-----CPAPELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHED 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 V-GLLPFGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 WNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 SGPTSTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPRVTCVVDVSEDD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C region; immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:1-19/Domain: signal sequence #status predicted <SIG>F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>F:159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.8%; Score 1504.5; DB 60.8%; Pred. No. 1.4e-78;
                                                                                                  SRWQQGNVFSCSVMHEALHNHYTQKSLSPG
                                                                                                                                                                                                                                               Ig gamma-2b chain precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.8
Best Local Similarity 60.8
Matches 290; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-475 <DE1>
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Use heavy chain V region precursor - human cipacies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S69339; Sr2664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A;Tille: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MuID:95262687
A;Reference number: S69339; MuID:95262687
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 < KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
Submitted to the EMBL: Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSHAFAYASYDFWGPGLLISVLSASTTPDKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYK 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 297
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                                                                                                                                                                                                                                                                                               3 WSCIILFLVATATCVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQ 62
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A;Accession: $72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                          homology
                                                                                                                                                                                                            Match 58.3%; Score 1467; DB 2; Length 4 Local Similarity 59.4%; Pred. No. 2e-76; les 282; Conservative 67; Mismatches 114; Indels
                                     A; Molecule type: mRNA
A; Residues: 1-472 <PAT>
A; Cross_references: EMBL:X69797
C; Superfamily: immunoglobulin C region; immunoglobulin
C; Keywords: immunoglobulin
F; 277-346/Domain: immunoglobulin homology <IMM>
Accession: S31459
Status: preliminary
                                                                                                                                                                                                            Query Match
Best Local S:
Matches 282,
  A; Accession:
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Accession: PC4436
R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Haradi, Biochem: Biophys. Res. Commun. 240, 566-572, 1997
A; Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp A; Reference number: JC5810; MUID:98063277
A; Reference number: JC444
A&AA>
C; Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against immunoglobulin homology
C; Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against immunoglobulin homology
F; 251-320/Domain: immunoglobulin homology **status predicted
F; 99/Disulfide bonds: interchain (to 98) **status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 SNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 NYNOKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYF--DVWGQGTL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCR----TPWVYAMDCWGQGTS 115
                                                                            Gaps
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                                                                                                                                                                                           5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMQWVKQAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
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Length 374;
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56.9%; Score 1432; DB 2; 59.9%; Pred, No. 1.5e-74; ive 28; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1426.5; DB : Pred. No. 3.7e-74; 80; Mismatches 94
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       Query Match
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sednences

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Gaps

9

Indels

Length 328;

260

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Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Racskovics, I;Sun, J;Butler, J.E.
J;Immunol. 153, 356-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence number: 147158; MUID:95015845
A;Reference number: 147158; MUID:95015845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roccession: 17318
A;Roccession: 17328
A;Roccession: 17328
A;Roccession: 17328
A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: 1gG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                            Query Match 50.1%; Score 1261; DB 2; Best Local Similarity 69.6%; Pred. No. 6.8e-65; Matches 231; Conservative 41; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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C;Species: Sus scrofa domestica (domestic pig)
C;Decies: 12-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Reference number: 147158; MUID:95015845
A;Accession: 147159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
   VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CP 253
                                                                      254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
                                                                                       A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124 C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                  LPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 433
                                                                                                                                                                                                                                       348 IPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKL 407
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                                                                                                                                                                                                                                                                                       434 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:23:13; Search time 53.64 Seconds (without alignments) 339.265 Million cell updates/sec

US-09-499-662-143
2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		homo	homo	homo	oryct	P01862 cavia porce			P22436 mus musculu	P01868 mus musculu	P20761 rattus norv	P01869 mus musculu	P03987 mus musculu	P01863 mus musculu	P20762 rattus norv	P01864 mus musculu	P01865 mus musculu	P20760 rattus norv	P01866 mus musculu	P01867 mus musculu	P01751 mus musculu	P01750 mus musculu	P01755 mus musculu	P03980 mus musculu	P01749 mus musculu	P01746 mus musculu	gnw	P01748 mus musculu	P06328 mus musculu	P01855 rattus norv	P01854 homo sapien	54	P01759 mus musculu	P23083 homo sapien
	a		GC1_HUMAN	GC2_HUMAN	GC4_HUMAN	GC_RABIT	GC2_CAVPO	GC3_HUMAN	GC1_RAT	GC3_MOUSE	GC1_MOUSE	GCB_RAT	GC1M_MOUSE	GC3M_MOUSE	GCAA_MOUSE	GCC_RAT	GCAB_MOUSE	GCAM_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	HV07_MOUSE	HV06_MOUSE	HV11_MOUSE	HV48_MOUSE	HV05_MOUSE	HV02_MOUSE	HV09_MOUSE	HV04_MOUSE	HV49_MOUSE	EPC_RAT	EPC_HUMAN	HV10_MOUSE	HV15_MOUSE	HV1G_HUMAN
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æ	Query Match		8.69	64.0	3	8	8	46.2	45.9	45.7	45.5	45.5	2	2	44.9	44.8	44.8	4	4	ŝ	$\sim$	22.3	21.0	20.8	20.8	20.5	20.3	20.0	19.5	19.4	19.3	19.3	19.1	19.1	19.0
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## ALIGNMENTS

MEDITINE-03203131, FULLMEN-0804334,
RA Schmidt W.E., Jung HD., Palm W., Hilschmann N.; RT "Three-dimensional structure determination of antibodies. Prin

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                                                                                                                                                          Deisenhofer J.;

"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Blochemistry 20:2361-2370(1981).

-I-MISCELLANDOUS: INTE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-I-MISCELLANDOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

-I-MISCELLANDOUS BU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
                              DISULFIDE BONDS.

MEDLINE=77070267; PubMed=1002129;

Dreker L., Schwarz J., Reichel W., Hilschmann N.;

Rule of antibody structure. The primary structure of a monoclonal 19G1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                   268-272.
-I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
RESIDUES 198, 267, 227.
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REMOVED POST-TRANSLATIONALLY.

K -> R (IN GLM(3) MARKER).

/FIId-VAR_003886.

D -> E (IN GLM(NON-1) MARKER).

/FIId-VAR_003887.

L -> M (IN GLM(NON-1) MARKER).
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MEDLINE-81208100; Pubmed-7236608;
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          iochemistry 9:3188-3196(1970).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003609; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
 Intrachain disulfide bonds.";
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PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
MIM; 147100;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-701-1986 (Rel. 01, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
1g gamma-2 chain C region.
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                                                                                                                                                                                                                                                                            gamma
                                                                                                                                                                                                                              TISSUE-Fetal liver;
MEDLINE-64235992; PubMed-6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hing-coding segments in human immunoglobulin gamme heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
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MEDLINE-83001943; PubMed=6811139;
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"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
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                        SEQUENCE OF 2-326 FROM N.A.
MEDILIPE-81219(521; pubmed-6804948;
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"Linkage and sequence homology of two human immunoglobulin gamma
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MEDLINE=80114419; PubMed=118920;
Hofmann T., Parr D.M.;
A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
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                                                                           chain constant region genes.";
Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL)
                                                                                                                                                                                                                    99-177 AND 310-326 FROM
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SEQUENCE OF 88-115 FROM N.A.
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                                                                                                                                                                                                                                                                                                            EMBO J. 1:403-407(1982).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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C -> S (IN REF. 3).
8310878668780F9C CRC64;
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Pred. No. 1.5e-103;
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91.8%; Pred. No. 1.5e.
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                              EMBL; J00230; AAB59393.1;
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MIM; 147110; -.
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MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-81157104; PubMed-6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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35940 MW; 3EDBD811EF208E7A CRC64;
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Immunoglobulin domain; Immunoglobulin C region.
  OCT-2001 (Rel. 40, Last annotation update) gamma-4 chain C region.
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91.8%; Pred. No. 8e-1
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam: PP00047; Ig; 3.
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SMART; SM00407; IGc1; 2.
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327 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-6135469; PubMed=1243651; Pratt D.M., Mole L.E.; Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit {\tt IgG} heavy chain from the recombinant
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-!- MISCELLANBOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
Ig gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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HILL R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.; (In) Killander J. (eds.); (In) Killander J. (eds.); Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
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Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
Sequence studies of the Fd section of the heavy chain of rabbit
immunoqlobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 88-266 FROM N.A.
MEDLINE-81299977; Pubmed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of tabbit 1gG: isolation of a cDNA encoding is heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    323 AA
                                                                                                                                             441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                               MARKERS AND REF. 5 THE E15 MARKER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 151:337-349(1975).
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HSSP; P01857; 1FC
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BIOChemistry 10:36-31(1971).

-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 UNBRED GUINEA PIGS.

PIN INBRED GUINEA PIGS.

HSSP; PO1772; 2FB4.

InterPro; IPR003507; 1g_-c1.

InterPro; IPR003507; 1g_-c1.

InterPro; IPR003600; 1g_-lke.

Pfam; PF00047; 1g; 3.

SMART; SM00410; 1G_-lke; 1.

SMART; SM00407; 1G_-ly.

PROSITE; PS00290; 1G_-MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-71058474; PubMed=4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
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the carboxyl-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGLYSLTSMYTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPEN 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
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SEQUENCE OF 227-311.
MEDILNE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                             MEDLINE-75036072; PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN).
CHAIN).
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69.8%; Pred. No. 3.9e-76;
Live 30; Mismatches 62; Indels 9;
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36074 MW; 5D231B7164D1FBA9 CRC64;
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                                                                                                 Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-(71). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
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                                                                             SEQUENCE OF 69-133 AND 312-329,
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                Biochemistry 13:4796-4803(1974)
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178
248
329 AA;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 383
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P01862;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last cannotation update)
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV
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                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                         I -> M (IN D11 MARKER).

-> A (IN RE15 MARKER).

-> E (IN REF. 2).

-> E (IN REF. 2).

-> E (IN REF. 3 AND 4).

-> E (IN REF. 5).

-> D (IN REF. 5).

-> E (IN REF. 5).

-> D (IN REF. 5).

-> E (IN REF. 5).

-> D (IN REF. 5).
                                                                                                                                                                                                                                                                                                                         DB 1;
                                                     domain; Immunoglobulin C region,
                                                                                                                                                                                                                                                                                                                        48.9%; Score 1231.5; DB 70.0%; Pred. No. 1.4e-77 tive 34; Mismatches 5
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Submitted (APR-1975) to the PIR data bank.
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MEDLINE=71058471; PubMed=5538606;
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                                    PROSITE; PS00290; IG_MHC; 1.
IGMULOGIODULIn domain; Immunog
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VARIANT 104 104 T
VARIANT 185. 185 T
CONFLICT 71 71 V
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 IPR003597; Ig_c1.
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InterPro; IPR003597; Ig_
Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
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187
201
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233
246
256
260
266
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323 AA;
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Matches 229
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GC2_CAVPO
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-1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                      435
318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-3 HEAVY CHAINS.
MISCELLANBOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN. MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                      Frangione B., Rosenwasser E., Prelli F., Franklin E.C.; "Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Biochemistry 19:4304 4308 (1980).
               378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
MEDLINE-82247835; PubMed=6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBUNI: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Franklin E.C.; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoqlobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region (Heavy chain disease protein) (HDC)
IGHG3.
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                                                                                                                          296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
                                                                                                                                                                                                           290 AA
                                                                                                            436 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-81021548; PubMed-6774747;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (DISEASE PROTEIN WIS)
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                         (Human)
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                                                                                                                                                                                                                                                                                                         Homo sapiens
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P01860;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
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T -> A (IN OMM).
/FTId=VAR_003893.
S -> N (IN OMM).
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F -> Y (IN OMM).
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Pred. No. 7e-73;
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46.2%; Score 1162; D
Best Local Similarity 91.4%; Pred. No. 7e-7
Matches 212; Conservative 11; Mismatches
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                                                                                                                       EMBL; J00231; AAA52805.1; ALT_SEQ
                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003507; Ig_like.
Pfam; PF00047; Ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00299; IG_MHC; 1.
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127
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                                                                                                                                       PIR; A02149; G3HUWI.
                                                                                                                                                     P01857; 1FC1.
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184
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MIM; 147120;
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MOD_RES
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438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                    Ig gamma-1 chain C region.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
                                                                                                                                                                                          Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 ---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
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CHAIN).
CHAIN).
                419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                         region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 1155; DB 1; Length 326; 63.4%; Pred. No. 2.4e-72; tive 52; Mismatches 60; Indels 10
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(WITH A HEAVY C
(WITH A HEAVY C
                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-1 chain C region.
                                                                             326 AA.
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Immunoglobulin domain; Immunoglobulin to NON_TER 1 1 1 CH1.
DOMAIN 197 CH1.
DOMAIN 98 112 HINGE.
                                                                                                                                                                                                                                                                                                CH1.
HINGE.
CH2.
                                                                             PRT;
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
                                                                                                                                                                                                          Gene 74:473-482(1988).
PIR; PS0017; PS0017;
HSSP; P01842; TRAB.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003997; Ig_c1.
Pfam: PF00047; ig: 3
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                       35946 MW;
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                                                                             STANDARD;
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219
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326
102
102
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220
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102
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176
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Best Local
                                                                           GC1_RAT
P20759;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-85027161; Pubmed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1gG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 5.5e-72;
                                                                                                                                                                                                                               update)
                                                                                                                                                                       01-A0G-1991 (Rel. 19, Created)
01-A0G-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update
Ig gamma-3 chain C region, secreted form.
                                                                                                                                   329 AA
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44; Mismatches
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PIR; B02156; GSNSC.
INESP: POLIBS7; IPC1.
INTERPRO; IPR003006; Ig_MHC.
INTERPRO; IPR003597; Ig_C1.
INTERPRO; IPR0035809; Ig_like.
Pfam; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
IMMUNOGIODULIN GOMBAN; IG_MHC; 1.
IMMUNOGIODULIN GOMBAN; IMMUNOGIODULIN C.
TEATROMEMBYANG; Alternative splicing.
294 EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK
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HINGE.
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65.0%;
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114 2
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Best Local Simi
Matches 215;
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GlycoSuiteDB; P01868; -.
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380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obbata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
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                             Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
II gamma-1 chain C region.
Mus musculus (Mouse).
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                                                                                                    440 WOOGNVFSCSVMHEALHNHYTOKSLSLSPGK 470
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Nucleic Acids Res. 6:3305-3321(1979).
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MEDLINE=73008889; PubMed=5073237;
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EMBL, V00793; CAA24174.1; --
EMBL, V00793; CAA24174.1; --
EMBL, V00793; CAA24175.1; --
EMBL, V00793; CAA24176.1; --
PIR, A02159; GIMS.
HSSP, P01842; 7FAB.
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Cell 18:559-568(1979).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation creation creation creation creation creation Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rot).
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MEDLINE-89232738; PubMed-3149946;
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Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
PIR; PS0018; PS0018.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-AVG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse)
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PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_lke.
Pfam; PF00047; ig; 3.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; Igc1; 2.
PROSITE; PS00290; Ig_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-44 FROM N.A.

MEDLINE=8222190; PubMed=65283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SECMENT OF MU CHAINS.
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                                                  Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
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MEDLINE-82115295; PubMed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl Eisenberg D., Wall R.;
Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
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4CC88343B7A1CE27 CRC64;
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CH3.
SEQUENCE OF 323-393 FROM N.A. MEDLINE-82197626; PubMed=6804950;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
Pfan; Pf60047; ig; 3.
SMART; SM00407; IGcl; 2.
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393 AA;
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218
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Gaps

10;

45.3%; Score 1140; DB 1; Length 393; 62.2%; Pred. No. 3.3e-71; cive 55; Mismatches 60; Indels 10

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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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                                                        258
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                                                                                                               319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPPVLDSDGSFFLYSKLTVDKS 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                    259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
         ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                     201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
                                                                                                                                                                                                                                                                                                                                                 23-027-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-3 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3;2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                 398 AA
                                                                                                                                                                                                                                              439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
                                                                                                                                                                                                                                                           Nucleic Acids Res. 11:6775-6785(1983).
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PTR; A02155; GNSW.
HSSP; P01857; 1FC1.
Interpro; IPR003060; Ig_MHC.
Interpro; IPR003507; Ig_C1.
Interpro; IPR003507; Ig_Like.
Frām; FR0047; Ig_1; SRART; SM00410; IG_LIke.
SMART; SM00410; IG_LIke.
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P03987;
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GC3M_MOUSE
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SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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                                                                                                                                                                                                                                                                                                                                                                    142 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 201
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                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                           202 LYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP--PCPAPELLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                     Length 398;
                                                                                                                                                                                                                        CF7F264B50A41B95 CRC64;
                                                                                                                                              (POTENTIAL)
                                                                                                 CH3.
POTENTIAL.
CYTOPLASMIC (POTENTIA
E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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64.7%; Pred. No. 4e-71;
tive 44; Mismatches 68;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-MAY-2000 (Rel. 39, Last annotation update)
19 gamma-2A chain C region, A allele.
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    Alternative splicing
                                                           HINGE.
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es 213; Conserv
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Transmembrane; P
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DOMAIN 1
DOMAIN 98
DOMAIN 114
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P01863;
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Best Local S:
Matches 213,
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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TRANSMEM
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EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
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P20762;
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MEDLINE-81223894; PubMed-6787604; Ollo R., Auffray C., Morchamps C., Rougeon F.; Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                          Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
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                                                                                                                                                                                                                                                                          de Preval C., Fougereau M.; "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Blochem. 30:452-462(1972).
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INTERCHAIN (WITH A HEAVY CHAIN)
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                                                                                Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                              MEDLINE=73056887; PubMed=4565406;
                                                                                                               MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; Pubmed=4831970;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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330 AA;
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60 GLYTLSSSVTVPSSTWSSQTVTCSVAHPATKSNLIKRIEPR----RPKPRPPTDICSCDDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=88166903; PubMed=3127222;
MEDLINE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Calftre P., Waldmann H., Calabi F.;
Sequence a rat immunoglobulin gamma 2c heavy chain constant region cDNN: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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      Immunoglobulin domain;
      Immunoglobulin C region.

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      DOMAIN
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2C chain C region.
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                                                                                                                                 299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
                                                                                              RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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HSSP: PD1857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
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01-FEB-1991 (Rel. 17, Last sequ
15-JUL-1999 (Rel. 38, Last anno
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                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                           437
                                           ||:|:||:||||||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
                                                                                                                                                                                 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-2A chain C region, B allele.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dognin M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Igla and Iglb allotyplc forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-1. MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                             378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
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MEDLINE-82037861; PubMed-6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
"Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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PIR; A02153; G2MSAB.
HSSP; P01857; 1FC1.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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GCAB_MOUSE
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Score 1126.5; DB 1; Length 335; Pred. No. 2.3e-70;

44.8%;

Query Match Best Local Similarity

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141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                 315 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
7; Gaps
                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK-----SCDKTHTCPPCPA
                                                                                                                                                                                        PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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Indels
70;
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                                                                                                                                                                                                                                                                                                                                                                                                                      435 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Mismatches
52;
Conservative
Matches 207;
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Search completed: August 14, 2002, 15:23:14 Job time: 687 sec

us-09-499-662-143.rsp

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August 14, 2002, 15:22:15; Search time 187.61 Seconds (without alignments) 433.386 Million cell updates/sec
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2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                            562222 seqs, 172994929 residues
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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SPTREMBL\_19:\* 1: sp\_archea:\* 2: sp\_bacteria:\* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mnes:\*
sp\_organe:\*
sp\_phage:\*
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sp\_phage:\* 9: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	O9d814 mis misculii	0991c4 mus musculu	Snm	mus	mus	Q91z05 mus musculu	Q95m34 equus cabal	Q96pq8 homo sapien	0921k1 mus musculu	Q96qa6 homo sapien	Q91wt3 mus musculu	Q9brv0 homo sapien	Q91wt1 mus musculu	Q91wr1 mus musculu	Q96bb9 homo sapien	рошо
20171111			O O	09D8L4	099LC4	Q99L25	Q99L31	Q9R1A4	091205	Q95M34	096PQ8	Q921K1	Q96GA6	Q91WT3	Q9BRV0	Q91WT1	Q91WR1	Q96BB9	Q96DK0
			DB	7	17	11	11	11	11	9	4	1	4	11	4	11	H	7	4
		Query	Length	473	463	473	468	437	473	337	701	278	614	481	200	481	488	597	496
	æ	Query	Match	65.1	64.7	63.1	62.1	57.0	56.4	50.2	49.9	39.2	36.8	35.4	34.1	33.2	32.6	32.3	31.9
			Score	1639,5	1628.5	1588.5	1562	1433.5	1420.5	1263.5	1257	986	927.5	890.5	859	836.5	820	812.5	804
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29bul0 homo	09bqb8	91a6	096aa6 homo	Q96k68 homo	Q96ey0 homo	9ka4	Q91wp5	091207 mus	1xe1	1x92	9m22	kx8	dcd9	Q9npp6 homo	1v67	24p9	298	2492	24r3	978	24q5	24r8	ds0 ]	Q924p5 mus	24q7	0924r4	2490	0924p8
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Q9BU10	Q9BQB8	099LA6	096AA6	Q96K68	Q96EY0	Q99KA4	Q91WP5	091207	Q91XE1	Q91 <b>x</b> 92	Q99M22	Q96KX8	Q9DCD9	O9NPP6	Q91V67	0924P9	Q9Y298	092402	Q924R3	095978	092405	Q924R8	080960	Q924P5	092407	0924R4	092400	Q924P8
4	4	11	4	4	4	11	11	11	11	11	11	4	11	4	11	11	4	11	11	4	11	11	4	11	11	11	11	11
597	597	484	618	464	613	487	479	486	480	482	479	496	426	416	143	143	150	142	145	157	143	146	159	144		145	143	140
0.3	0.1	0.1	6.6	9.2	9.1	8.8	8.5	7.8	7.4	6.1		5.5	4.0	3.1	1.6	1.1	6.0	0.5	0.4	0.2	8.6	9.7	7.6	9.7	7.6	9.5	9.4	9.4
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17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Best Local Similarity 63.88
Matches 301; Conservative
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SMART; SM00409; IG; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GQGLEWIGKIGPGSGSTYINEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARS-G 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GOGLEWMGEIDPSDSYTNYNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 WNSCALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.1%; Score 1639.5; DB 11; Length 473; 63.9%; Pred. No. 8.2e-129; ive 69; Mismatches 94; Indels 9;
Strausberg R.;
Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                       Matches 304; Conservative
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            099LC4;
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61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.7%; Score 1628.5; DB 11; Length 463; 63.8%; Pred. No. 6.6e-128; ive 71; Mismatches 89; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888 aAH03888.1;
InterPro; IPR003599; Ig.
InterPro; IPR03509; Ig.
InterPro; IPR003609; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR0047; Ig_ 3.
SMART; SM00409; IG; 2.
SMART; SM00400; IGv; 1.
SMART; SM00410; IG_1; 2.
SMART; SM00410; IG_1; 1.
SMART; SM0410; IG_1; IG_1; IG_1; 1.
SMART; SM0410; IG_1; IG_1
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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96352328B3332ADB CRC64;

51661 MW;

468 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
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                                                                                                                                                                          Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.1%; Score 1588.5; DB 11; Length 473; 63.6%; Pred. No. 1.5e-124; ive 60; Mismatches 106; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
R Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC003878; AAH03878.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003509; Ig.
R InterPro; IPR003506; Ig_AMC.
R InterPro; IPR003506; Ig_AMC.
R InterPro; IPR003596; Ig_V.
R SMART; SM00409; IGC1; 3.
R SMART; SM00409; IGC1; 3.
R SMART; SM00409; IGC1; 3.
R SMART; SM00409; IGC1; 16.
R SMART; SM00409; IGC1; 16.
R SMART; SM00409; IGC1; IGC1; 17.
R SMART; SM00409; IGC1; IGC1; 17.
R SMART; SM00409; IGC1; IGC1; 17.
R SMART; SM00409; IGC1; IGC
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
SMART; SM004106; IG_LIKe; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09121;
01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                                                                                    Best Local Similarity
Matches 302; Conser
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                                                                                                                                   Query Match
Best Local $
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SEQUENCE FROM N.A.

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its 11ght and heavy chains) and construction of a single chain antibody (ScFY).";

Sübmitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF153372; AAAQ4043.1; -.

HSSP, P01642; 7FAB.

InterPro; IPR003606; Ig_like.

InterPro; IPR003506; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
                                                                                                                                                                    GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYCARNRD 120
                                                                                                                                                                                        Gaps
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                                                                                 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                           WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                           YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                        241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Sciurognathi; Muridae; Murinae; Mus
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  Length
                                         Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMA1 HENYY CHAIN OF MAB7 (FRAGMENT).
MUS MUSCULUS (MOUSE).
; Score 1562; DB 11;
; Pred. No. 2.5e-122;
61; Mismatches 108;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
62.1%;
62.9%;
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
                        Best Local Similarity 62.9
Matches 297; Conservative
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437 AA;
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                                                                                                                                                                                                                          228 --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 285
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                                                                                                                                                                                                                                                                                            141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                      319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                                                                                                       Gaps
                                                                                                21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNYN 80
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Wataryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                  17;
  DB 11; Length 437;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -
Hypothetical protein.
SEQUENCE 473 AA; 51946 WW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al protein.
473 AA; 51946 MW; CF625F008932AF12 CRC64;
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                                                  96;
                         Pred. No. 1.3e-111;
57.0%; Score 1433.5;
59.1%; Pred. No. 1.3e
                                             72; Mismatches
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Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch G., Sheoran A., Holmes M., Richards C., Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).

EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                   ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD
                         KT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                         298 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                           421 APVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 473
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Last sequence update)
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CHAIN CONSTANT REGION
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         240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGGSFFLYSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                           NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISKAKGQPREPQYYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                   "Targeting tissue factor on tumor vascular endothelial cells ar cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL; AF272774; AAKS6866.1; - SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHFALHNHYTQKSLSLSPGK 701
                                                                                                                                                                                                                                                                                                                                                                     Length 701;
                                                                                                                                                                                            Homo sapiens (Human).
Butelé subraryora: Metazoa; Chordata; Craniata; Vertebrata; Buthelé Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   Score 1257; DB 4;
Pred. No. 1.4e-96;
2; Mismatches 0;
                                                         LIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                   096P08;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence upda
01-DEC-2001 (TrEMBLrel. 19, Last annotation up
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
                                                                                                                             Æ
                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                MEDLINE=21477448; PubMed=11593034;
                                                                                                                                                                                                                                                                                                                                                                   49.9%;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.1
Matches 230; Conservative
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           Z., Garen A.;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                          096P08
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                                                                                                                                                                          YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSNNW--YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD 357
                                        Gaps
                                                                                                                9
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                                                                                                                                                        GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                               181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Indels
  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --------CDKTHTCP------CDKTHTCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.8%; Score 927.5; DB 4;
36.6%; Pred. No. 4.3e-69;
11ve 85; Mismatches 166;
Score 986; DB 11;
Pred. No. 1.8e-74;
                                                                                                                                                                                                                                                                                                                                                                                       Ž
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN (PROTEIN FOR MGC:15420).
                                        32;
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39.2%;
67.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.8'
Best Local Similarity 36.6'
Matches 211; Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                      187;
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121 SYSSCONDYXYYYMDVWGKGTTVTVSSASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK---------DTLM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DXS---NNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPSQDVTV------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1SRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEP
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-PROSTATE;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.1%; Score 859; DB 4;
41.1%; Pred. No. 1.7e-63;
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Hypothetical protein.
SEQUENCE 500 Am.
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R InterPro; IPR003597; Ig_c1.
R InterPro; IPR003600; Ig_like.
R InterPro; IPR003060; Ig_like.
R InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00406; IGv; 1.
PROGRAMMET; SM00410; IG_like: 1.
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                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                   (Human)
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Best Local Similarity
Matches 206; Conserv
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                  470
                                                                                                           463
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                                                                                                                                                                                                                                             Q9BRV0;
                                                                                                                                                                                                                      Q9BRV0
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                                                                                                                                                    475
                                                                                                                                                                                                                    -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                               PSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 QDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHINISE
                                                                                                                                 SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 IEKTISKAKGOPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGO---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 LIGIIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.4%; Score 890.5; DB 11; Length 481; 42.9%; Pred. No. 3.8e-66; Live 72; Mismatches 172; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-COLON;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOLON;
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.0 KDA PROTEIN.
BINE MUSCULUS (Mouse)
                                                                                                                                                                                                                                                                                                          431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Best Local S
Matches 207
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Q91WT3
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32.6%; Score 820; DB 11; 39.4%; Pred. No. 3.1e-60; Conservative 84; Mismatches 177;
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                  PRT;
                PRELIMINARY;
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLSPGK 470
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IDRLSGK 470
                                                                                                                                                                              TISSUE=KIDNEY;
Strausberg R.;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 192;
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                             Q91WR1;
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                091WR1
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    091WR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GGGWAFDYWGQGTTLTVSSEPAREPTIYPLT-FPQALSSDPVIIGCLIHDYFPSGTMNV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            091WT1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                       33.2%; Score 836.5; DB 11; Length 40.5%; Pred. No. 1.3e-61; Live 72; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                       Straugherg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
Hypothetical protein.
SEOUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                                                                                                                  481
                                                                                                                                                  PRT;
                                                     450 VMHEALHNHYTQKSLSLSPGK 470
                                                                     | ||||| :||:: ||
462 VGHEALPLAFTQETIDRLAGK 482
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.2%
Best Local Similarity 40.5%
Matches 195; Conservative
                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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121 YSNNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 -PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 ESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 53.0 KDA PROTEIN.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia; Euthoria, Chordata, Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 QELNVNCPGICSPPTTPPPPSCO----PSLSLQRPALED-LLLGSDASITCTLNGL--RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
HOMO Sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC013539; AAH13539.1; -. Hypothetical protein. Protein: 22964 MW; F12068460B400B9D CRC64; SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
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18;
                                                                                                                                                                                                                                                                                                               176 PVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPS 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                               61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARN-R 119
                                                                                                                                                                                                                                                                                                                                                      120 DYSNNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 NKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPPSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF 428
                                                                                                                                                                                                                                    231 N-----TKVDKRVEPKS------CDKTHTCP----TKVDKRVEPKS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 GSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSOSMFTCRVDHRGLTFQQNASSMCV
                                                                                                                                                                             Query Match 32.3%; Score 812.5; DB 4; Length 597;
Best Local Similarity 32.5%; Pred. No. 1.7e-59;
Matches 189; Conservative 95; Mismatches 179; Indels 119;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                SEQUENCE FROM N.A.
TISSUB-PRIMARY B-CELLS FROM TONSILS;
Strauaberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 -----PCPAPELLGGPS-----
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Search completed: August 14, 2002, 15:22:16 Job time: 684 sec

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August 14, 2002, 15:15:37 ; Search time 230.21 Seconds (without alignments) 226.770 Million cell updates/sec
                                                                                                                                                                                        US-09-499-662-145
2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                    747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5.
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Perfect score:
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1: /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1980.DAT:\*
2: /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:\*
3: /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:\*
4: /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:\*
5: /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:\*
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7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
9: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
110: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
111: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
112: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\*
113: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\*
114: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\*
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117: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
118: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
119: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Humanised HFE7A de	Humanised HMFG-1 h
QΙ	AAW90934	AAW90933	AAW83037	AAB14779	AAW90929	AAW90935	AAW83036	AAB14776	AAW90926	AAW90936	AAM52156
DB	21	21	19	21	21	21	19	21	21	21	22
% Query Match Length DB	470	470	470	470	470	470	470	470	470	470	731
% Query Match	100.0	6.66	8.66	8.66	8.66	8.66	99.3	99.3	99.3	99.5	93.3
Score	2517	2515	2512	2512	2512	2512	2499	2499	2499	2497	2348.5
Result No.	н	7	ю	4	S	9	7	<b>a</b>	6	10	11

12	2348.5	93.3	741	22	AAM52159	
13	2343.5		729	22	AAM52158	HMFG-
14	2343.5		739	22	AAM52161	HMFG-
15	2337.5		730	22	AAM52157	HMFG-
16	2337.5		740	22	AAM52160	Humanised HMFG-1 h
17	2303	91.5	652	19	AAW48650	in of
18	2290.5		465	22	AAB72228	
19	2285.5		464	22	AAB72232	Humanised 323/A3 (
20	2285		470	21	AAB08026	A dimeric anti-CD2
21	2284	20.7	466	22	AAE03755	Chimeric 2403 IgG
22	2254		476	20	AAW88464	Monoclonal antibod
23	2253.5		481	13	AAR24442	Sequence of antibo
24	2246	•	472	20	AAY50166	Human reshaped F19
25	2232		476	14	AAR31023	Antibody D heavy c
56	2231.5	88.7	583	22	AAB83156	Ganglioside GM2 an
27	2230		449	14	AAR43339	Completely humanis
58	2230	98.6	449	19	AAW49816	Amino acid sequenc
59	2200.5		467	22	AAB36210	Human immune syste
30	2198.5	87.3	452	20	AAY29458	Recombinant immuno
31	2198.5	87.3	452	21	AAB30322	Humanised anti-IL-
32	2198.5	87.3	452	21	AAY77766	Humanised anti-IL-
33	2198		472	20	AAY50157	Chimeric mouse/hum
34	2191		592	22	AAB83838	Amino acid sequenc
35	2189.5		452	19	AAW69316	Anti-IL-8 humanise
36	2188		474	22	AAU14177	Human novel protei
37	2188	86.9	595	20	AAW86003	Anti-5T4 single ch
38	Ġ		473	22	AAG64475	Human type antihum
39	ς.		473	22	AAG64471	Human type antihum
40	2183.5		475	22	AAG63640	Amino acid sequenc
41	<u>~</u> :		473	22	AAG64469	type
42	7		468	20	AAW85689	D9D10 heavy chain
43	2177	86.5	711	20		MoTAbII fusion pro
44	2171.5		473	22	AAG64473	Ω
45	16		470	13	AAR22757	Reshaped CAMPATH-1

## ALIGNMENTS

Takahashi T; Tamaki I, Nakahara K, Haruyama H, WPI; 2000-258930/23. Serizawa N, 

N-PSDB; AAA11645

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

English. Claim 2 ; Page 174-176; 263pp;

Intortion describes a nover numerized anti-ras antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ilgand system by binding to Fas on the cells with an abnormal Fas/Fas ilgand system by binding to Fas on the cells with an abnormal Fas/Fas ilgand system by binding to Fas and prevents for anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive cinhibition of ligand binding. (I) are used to treat and/or prevent clubes exphematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autohimune hemolytic anemia, sterility, mysathenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, hepatisis (fulminant, chronic, viral (B), C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in mormal cells. They about the active site of Fas, i.e. they minic murine disease models. (I) act on the active site of Fas, i.e. they minic the attive ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention. This invention describes a novel humanized anti-Fas antibody-like

470 AA; Sequence

ö ö Length 470; Indels 100.0%; Score 2517; DB 21; 1larity 100.0%; Pred. No. 4.4e-143; Conservative 0; Mismatches 0; I) Local Similarity Best Local Sim. Matches 470; Query Match

9 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP ò

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g ð

YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 g ð

ö g

241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 qq ð

YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360 301 301 g ò

KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

361

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361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420 g

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AAW90933 RESULT

À. AAW90933 standard; Protein; 470

AAW90933;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 1 protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolecotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

05-APR-2000.

99EP-0307711. 29-SEP-1999; 98JP-0276881. 98JP-0276882. 30-SEP-1998;

30-SEP-1998;

(SANY ) SANKYO CO LTD.

A STATE OF COLORO COLOR

Takahashi T; Nakahara K, Tamaki I, Serizawa N, Haruyama H,

WPI; 2000-258930/23. N-PSDB; AAA11644.

treating or preventing e.g. apoptosis selectively in New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

Another than the state of the s disease, autoimmune hemolytic anemia, sterility, mysthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B. C or D) or alcoholic), and transplant rejection. (I) selectively This invention describes a novel humanized anti-Fas antibody-like

location/Qualifiers

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Query Match
    ö
inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu I which is described in the method of the invention.
                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                      121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                        301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                    KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                                                                                                                                                                                    GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                  241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                         Gaps
                                                                                                                                                            1 MGWSCIILFLVATATGVHSOVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                       WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune heemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease;
                                                                                                                     Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombopenia purpura; insulin-dependent diabetes; allergy; actopy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFE7A; monoclonal antibody; mouse; Fas; humanised antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis, HFE7A; autoimmune disease, Hashimoto's disease, systemic lupus erythematosus, graft versus host disease;
                                                                                                                                         Indels
                                                                                                                  Score 2515; DB 21;
Pred. No. 5.8e-143;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Fas humanised antibody HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW83037 standard; Protein; 470 AA
                                                                                                                  99.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                             Best_Local Similarity 99.8
Matches 469; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Best Local
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chain of murine anti-human Fash monoclonal antibody HFETA. It includes humanising R44G and A76T amino acid substitutions that are includes humanising R44G and A76T amino acid substitutions that are conserved in the human Ig6 heavy chain. Host Escherichia coli pythophy3 SANK 70298 harbors plasmid pythophy3 carrying a fusion fragment of the humanised HV type HFETA heavy chain and DNA concoding human Ig61 constant region (see AAV70080), and is deposited as FERW BP-6273 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve FasyFas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Solgreen syndrome, permitotious anaemia, Addison's disease, scleroderma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the HV type humanised heavy
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T;
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                                                                             20..470
/label- Mat_protein
20..140
/label- Variable
                                                     label - Sig_peptide
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S, Shin Y,
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/label= Constant
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/label- CDR_H1
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/label= C
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25-JUN-1997;
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DB 19; Length 470;

Score 2512; DB 19; Pred. No. 8.8e-143;

99.88;

Best Local Similarity

4

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08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                           Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Ilgand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody ^{\rm -}
                                                                                                                                                                                  240
                                                                                                                                   240
                                                GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                  YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                  KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
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                                                                                                                                                                                                                            Gaps
                       9
                                                                                                                          MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                  WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                          ..
                                                                                                                                                                                                                                                             LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Indels
                                                                                                                                                                                                                                                                                                                                                             Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
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0
Mismatches
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                                                                                                                                                                                                                                                                                                            AAB14779 standard; Protein; 470
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                                                                                                                                                                                                                                                                                                                                             (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       - Mus musculus.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-485645/43.
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468;
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Matches
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA. or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFFEFVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 yvdgvevhnaktkpreegynstyrvvsvltvlhgdwlngkeykckvsnkalpapiektis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2512; DB 21;
Pred. No. 8.8e-143;
2; Mismatches 0;
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Best Local Similarity 99.6%;
Matches 468; Conservative
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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC digada system, by binding to Fas on the cell surface, and prevents

apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

antidabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, darmatological, immunosuppressive, thyromimetic,

antinrheumatic, nephrotropic, antilnertility, neuroprotective,

antiarterioscleroric, cardiant and hepatropic activity. (I) induce

antinrheumatic, nephrotropic, antilnertility, neuroprotective,

antinrheumatic, nephrotropic, antilnertility, neuroprotective,

cantinplicion of ligand binding (I) are used to treat and/or prevent

continuation of ligand binding (I) are used to treat and/or prevent

continuation of ligand binding (I) are used to treat syntem, especially systemic

continuation of ligand binding (I) are used to treat syntemic

continuation of ligand binding (I) are used to treat syntemic

continuation disease, slorgen synteme, permittic, propalatic

continuation disease, slorgen synteme, goodpasture syntemic

continuation disease, slorgen syntemia, sterility, myasthenia gravis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

continuation disease models. (I) act on the active site of Fas, i.e. they minic

cells. They bind to both human anti-murine murine fas, so can be evaluated in

continuation a human anti-murine antibody response. This sequence represents

continuation anti-murine antibody HERFA designed heavy chain which is used in

continuation a human anti-murine antibody response. This sequence represents
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Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i
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2; Mismatches
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Matches 468; Conser
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                                                                                                     Synthetic
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                            240
361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                            241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                            YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAW90935 standard; Protein; 470 AA
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98JP-0276882.
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continuous in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirtheumatic, nephrotropic, antilnfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding (I) are used to treat and/or prevent capptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding (I) are used to treat and/or prevent capsus host disease, slorgen's syndrome, permitticity, graft versus host disease, soloroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, anitiple sclerosis, Basedow, sisease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chornic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in captine a human anti-murine antibody response. This sequence represents the native ligand do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents which is described in the method of the invention.
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470 AA; Sequence

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                                                                                                                            61 ggglewmgeidpsdsytnyngkfkgkatltvdtststaymelsslrsedtavyycarnrd 120
                                                                                                                                                                                                                                                      241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                   YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                     KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                           Gaps
                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                  121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                     181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                 ;
  Length 470;
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  Score 2512; DB 21;
Pred. No. 8.8e-143;
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                           2; Mismatches
99.88;
99.68;
                           Conservative
  Query Match
Best Local Similarity
               Best Local Simi
Matches 468;
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Anti-Fas humanised antibody HFE7A heavy chain.

HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic luque erythematosus; graft versus host disease; Sjogrem syndrome; pernicious anaemia; Addison's disease; sclerodernma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; attopicsclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Homo sapiens. Synthetic.

20..470 /label= Mat\_protein /label= Sig\_peptide Location/Qualiflers 20..140 /label- Variable 141..464 /label= Constant "claim 9" "claim 9" 50..54 /label= CDR\_H1 /label= CDR\_H2 CDR\_H3 118..129 /label= Cl /note= 118..12 /note= Peptide Protein Region Region Region Region Region Key

/note= "claim 9" NEW YORK OCCOUNTS OF THE PROPERTY OF THE PROPE

AU9859701-A 08-OCT-1998 98AU-0059701 30-MAR-1998;

97JP-0276064. 97JP-0082953. 97JP-0169088. 08-OCT-1997; 25-JUN-1997; 01-APR-1997;

(SANY ) SANKYO CO LTD.

un O, Kimihisa I; Tohru T; Jun O, S, Shin Y, Hiroko Y, Nobufusa Hidevuki H, Masahiko O, Akio S.

WPI; 1998-543440/47. N-PSDB; AAV70079

used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, New antibodies and proteins bind conserved epitope of Fas antigen myocarditis, hepatitis and AIDS

Claim 22; Page 212-213; 292pp; English.

This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. colipgist7A62 SarX 73397 harbors plasmid pgHSL7A62 carrying a fusion fragment of the humanised VD type HFB7A heavy chain and DNA encoding human IgGl constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFB7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of antiboting Fas induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to

> AAW83036 standard; Protein; 470 AAW83036 RESULT

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(first entry) 15-MAR-1999

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AAW83036;

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                                                                                                                                                                                                                                                                                                                                                  GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                  121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allerqise, atopy, arteriosclerosis, mayocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
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                                                                                                                                                                                                            Length 470;
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                                                                                                                                                                                                         99.3%; Score 2499; DB 19;
99.1%; Pred. No. 5.3e-142;
ive 2; Mismatches 2;
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                                                                                                                                                                                                                                          Conservative
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Chimeric - Homo sapiens.
                                                                                                                                                                                                                         Similarity
                                                                                                                                                              470 AA;
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Matches 466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB14776;
                                                                                                                                                              Sequence
                                                                                                                                                                                                         Query Match
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA.

To humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atcept, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                             Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAKGOPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2499; DB 21; Length 470;
Pred. No. 5.3e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Scor.
99.1%; Pred. No. ...
2; Mismatches
                                                                                                                                                                                                        Claim 21; Page 95-96; 139pp; Japanese.
                                           98JP-0276883
             99JP-0278301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 466; Conservative
                                                                       (SANY ) SANKYO CO LTD
                                                                                                    WPI; 2000-485645/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             470 AA;
                                                                                                                                                                             anti-Fas antibody
                                                                                                                  N-PSDB; AAA72159
                                           30-SEP-1998;
             30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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RESULT AAW90926

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Length 470;

DB 21;

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; antiallergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                    Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example reference 15; Page 134-136; 263pp; English.
                                                                   Humanised HFE7A designed heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                   Nakahara K,
AAW90926 standard; Protein; 470 AA.
                                                                                                                                                                                                                                                                                                    99EP-0307711.
                                                                                                                                                                                                                                                                                                                           98JP-0276881.
98JP-0276882.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Serizawa N, Haruyama H,
                                                                                                                                                                                                                                                                                                                                                              (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA11597
                                             08-AUG-2000
                                                                                                                                                                                                                                                                                                     39-SEP-1999;
                                                                                                                                                                                                                                                                                                                            30-SEP-1998;
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                                                                                                                                                                                                                                                       EP990663-A2
                                                                                                                                                                                                                                  Synthetic.
                        AAW90926;
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New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents capoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between capoptosis in cells with a normal system, by inhibiting binding between capoptosis in cells with a normal system, by inhibiting binding between capoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding (I) are used to treat and/or prevent capoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding (I) are used to treat and/or prevent capoptosis by binding to cell surface Fas or inhibit it by competitive inhibit in apoptosis system, especially systemic capoptosis by binding to cell surface Fas or inhibit it by competitive canemia, statistic architity, myasthenia system; cutsis host disease, Slorgen's syndrome, pernicious or hypoplastic versus host disease, Slorgen's syndrome, pernicious or hypoplastic canemia, addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in cantine disease models. (I) act on the active site of Fas, i.e. they minic inducing a human anti-murine antibody response. This sequence represents a humanised anti-marine antibody HERPA designed heavy chain which is used in the invention.

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Sequence
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                                                                                                                            61 GQGLEWMGEIDPSDSYTNYNOKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                               121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                      361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420
                               Gaps
                                                               1 MGWSCIILFLVATATGYHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                               antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                            241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                               Indels
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Score 2499; DB 21;
Pred. No. 5.3e-142;
                               2; Mismatches
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98JP-0276882.
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                                  Conservative
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                Similarity
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                               Matches 466;
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Best Local S
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361 kakgqprepqvytlppsreemtkngvsltclvkgfypsdiavewesngqpennykttppv 420

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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosis by binding to cell surface Fas or inhibit it by competitive
contains by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
contains, Addison's disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
corsus host disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
cdependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis hepatitis (fulminant, chronic, viral
colls. They bind to both human and murine Fas, so can be evaluated in
multiple apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
which is described in the active site of Fas, i.e. they mimic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                             e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l anti-Fas antibody, useful for treating or preventing or autoimmune disease, induces apoptosis selectively i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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                 Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which is described in the method of the invention
                 Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2497; DB 21
Pred. No. 7e-142;
; Mismatches 2
                                                                                                                                                 cells with abnormal Fas-Fas ligand systems
                 χ,
                                                                                                                                                                                     Claim 2; Page 188-189; 263pp; English.
                 Nakahara
                                                                                                           New humanized anti-Fas antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
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                 Haruyama H,
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                                                   WPI; 2000-258930/23.
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               Serizawa
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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytocoxic portion having endonucleolytic activity, exemplified by AAM52154-3ABM5168 and encoded by ABA02682-ABA02788. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                            Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity follymorphic epithelial mucin, and cytotoxic portion having endouncleolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
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                                                                                          A
                                                                                          AAM52156 standard; Protein; 731
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02-OCT-2000; 2000US-237159P.
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                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                    Homo sapiens.
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Matches 437;
                                                                                                                                                                                                                                               Synthetic
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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

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KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

301 301 361

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1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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                                                                                                                                                                                                                                                                                                                                                                Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                    300
301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
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                                   KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                             Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity f polymorphic epithelial mucin, and cytotoxic portion having
                                                                                                                                                                               LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                             Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Figure 10; 176pp; English.
                                                                                                                                                                                                                                                                  Protein; 741 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-2000; 2000GB-0008049, 02-OCT-2000; 2000US-237159P.
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                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endonucleolytic activity
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                                                                                                                                                                                                                                                                AAM52159 standard;
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Synthetic.
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Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
300
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                                                      121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                 237
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for
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                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                               YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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2000US-237159P
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02-OCT-2000;
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Gaps

3;

Indels

Length 741;

DB 22;

93.3%; Score 2348.5; DB 2: 93.0%; Pred. No. 8.9e-133; ive 20; Mismatches 10;

Conservative

Similarity

Local Simil thes 437; (

Matches

Query Match

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Homo sapiens
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Matches 436;
   RJ;
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    Young
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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody; polymorphic epithelial mucin; PEM1; use; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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                                                                                                                                                       GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
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                                                                                                    10; Indels
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                                                                                  DB 22;
                                                                                 93.1%; Score 2343.5; DB 2 93.0%; Pred. No. 1.7e-132;
                                                                                                    Mismatches
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2000US-237159P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                   436; Conservative
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02-OCT-2000;
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                                                       Sequence
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Matches
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I; human; cytostatic; cancer; apoptosis.
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                                         Novel compound used to treat cancer has target cell-specific por comprising humanised monoclonal antibody having specificity for polymorphic epithelial macin, and cytotoxic portion having endonucleolytic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2343.5; DB 2 Pred. No. 1.8e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                  Claim 20; Figure 12; 176pp; English.
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93.0%;
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2001-662969/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                      739 AA;
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Search completed: August 14, 2002, 15:15:38
Job time: 836 sec

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92.9%; Pred. No. 4e-132;
.ive 20; Mismatches 10; Indels
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                                                                                                   03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
                                                                           26-MAR-2001; 2001WO-GB01324
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Matches 435; Conser
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                        WO200174905-A1
                                                  11-OCT-2001
Synthetic.
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Sequence 9, 1
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FILING DATE:
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88.7%; Pred. No. 5.2e-159;
iive 20; Mismatches 28;
US-09-679-397-2
PCT-US93-07832-23
US-08-437-642B-23
US-08-1247-352-3
US-08-1247-352-3
US-08-1247-352-3
US-08-147-101A-7
US-08-147-101A-7
US-08-049-672A-4
US-08-397-411-7
US-08-487-550-12
PCT-US96-10043-9
US-08-461-968A-5
US-08-461-968A-5
US-08-461-968A-5
US-08-461-968A-5
US-08-461-968A-5
US-08-480-012
US-08-480-012
US-08-480-036-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ROTHWELL, FIGG, ERNST 6 KURZ STREET: 555 THIRTEENTH ST. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEX: (202) 783-604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 88.78
Matches 422; Conservative
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1 MGWSCIILFLVATATGVHSQ.......MHEALHNHYTQKSLSLSPGK 470
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
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Compugen Ltd
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US-09-049-672A-8

US-09-026-985-71

US-09-485-737B-67

US-09-485-737B-67

US-09-485-737B-67

US-09-485-737B-22

US-08-437-642B-22

US-08-437-642B-22

US-08-173-450-8

US-08-109-207C-14

US-09-109-207C-14

US-09-206-005-14

US-09-296-005-14

US-09-296-005-14
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US-09-109-207C-18
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US-09-054-255-2
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                                      GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1 MDWTWRFLFVVAAATGVQSQMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYAISWVROAP
                           61 GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CC, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCE: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/458,516 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08458516 Patent No. 5777085 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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CITY: San Francisco
STATE: California
COUNTRY: USA
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linear
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TOPOLOGY: lin
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119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
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                                                       Gaps
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                                                                                                         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY
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APPLICANT: Tang, Y. Tom
APPLICANT: Tue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
     Length 449;
                                                    Indels
Query Match 88.6%; Score 2230; DB 1; Best Local Similarity 92.9%; Pred. No. 6.8e-159; Matches 419; Conservative 15; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A FILLING DATE: HEREWITH CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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MEDIUM TYPE: Diskett
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South San Francisco
California
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US-09-026-985-71
                           COUNTRY:
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Batent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                 28; Indels
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                                     NAME: CELTONE, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Genentech, Inc.
1 DNA Way
                         ATTORNEY/AGENT INFORMATION:
                                                                                                                               INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
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                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
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| LIBRARY: LUNGTUT11
| CLONE: 2747531
| US-09-049-672A-8
APPLICATION NUMBER: FILING DATE:
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US-09-027-449-71
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80 NQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGTLVTV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.3%; Score 2198.5; DB 3
89.8%; Pred. No. 1.5e-156;
tive 28; Mismatches 17;
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 20-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                   PRIOR APPLICATION PATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-3a-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34.659
REFERENCE/DOCKET NUMBER: P1085R3-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAME : 650/225-530
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 452 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 406; Conservative
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APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: 05/09/485,737B
CURRENT APPLICATION NUMBER: PCT/2P
PRIOR FILING DATE: 1998-06-14
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEC ID NOS: 104
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.5%; Score 2177; DB 4;
88.2%; Pred. No. 6.5e-155;
live 20; Mismatches 31;
   421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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US-09-485-737B-90
; Sequence 90, Application US/09485737B
                                                                                                             Sequence 67, Application US/09485737B Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: SYNTHETIC US-09-485-7378-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.5%
Best Local Similarity 88.2%
Matches 410; Conservative
                                                                                                                                                       GENERAL INFORMATION:
                                                                                           US-09-485-737B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.3%; Score 2198.5; DB 4
89.8%; Pred. No. 1.5e-156;
iive 28; Mismatches 17;
                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPATIN (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/09/026,985
20-Feb-1998
Sequence 71, Application US/09026985 Patent No. 6133426 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 89.8 Matches 406; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650/952-9881
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US-09-026-985-71
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                                                                                                                                                                                                                                                                                      126 YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA 185
                                                                                                                                                                                                                                                                                                                                                                                   186 LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQ 362
                                             Gaps
                                                                                          6 IILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLE 65
                                                                                                                246 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
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                                               4
Length 468
                                             Indels
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KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P07
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 454 amino acids TYPE: Amino Acid
        south San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 89.2%;
Matches 405; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   650/952-9881
                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-934-373C-22
                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                            COUNTRY:
                                             STATE:
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                                    TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT APPLICATION NUMBER: EPO 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
NUMBER: PEO 10 NOS: 104
SEQ ID NO 90
SEQ ID NO 90
LENGTH: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                86.5%; Score 2177; DB 4; Length 711;
88.2%; Pred. No. 1.1e-154;
tive 20; Mismatches 31; Indels
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APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
WUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/07934373C Patent No. 5821337 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                 COTHER INFORMATION: SYNTHETIC US-09-485-7378-90
                          APPLICANT: Buyse, Marie-Ange
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.2 Matches 410; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-934-373C-22
                                                                                                                                                                                                                                                                                                   TYPE: PRT
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137 TVSSASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
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; Pred. No. 1.3e-153;
18; Mismatches 28;
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFFICATION NUMBER: US/07/934,373C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                   WinPatin (Genentech)
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241 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
                                                                                                                                                                                                                                                           301 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
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                                                                                                                                                                                                                             SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                                                   EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/Ms-r-COMPATE: Da+1+-COMPATE: DA+1+-COMPA
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Best Local Similarity 89.2%; Pred. No. 1.3e-153;
Matches 405; Conservative 18; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
OCRRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
PRIOR APPLICATION DATA:
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMBER: 07/934373
21-AUG-1992
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION
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APPLICATION NUMBER: C
FILING DATE: 21-AUG-1
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PCT-US93-07832-22
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
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; Pred. No. 1.3e-153;
18; Mismatches 28;
                                                                                                                                                 APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
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FILING DATE: 17-NOV-1993
RAIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
RAPPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                              Sequence 22, Application US/08437642B Patent No. 6054297 GENERAL INFORMATION:
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NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P070:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/252-1994
TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
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STATE: California
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Matches 405; Conservative
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US-08-437-642B-22
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                                 US-08-437-642B-22
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TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
                                                                                                                                                                         LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                                                                        EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
                                                                                                                                                                                                                                                                                                   377 SREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLTVD 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARCARITEL
APPLICANT: KACZONEK, MICHEL
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: SOURCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: D.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER EALCABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/AKS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR.1997
CLASSIFICATION NUMBER: FF 94/10566
FILING DATE: 02-SEP-1994
ATONNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN ERESTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08793450 Patent No. 6312690
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amino acid
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MOLECULE TYPE: protein
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STATE:
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Sequence 14, Application US/08887352B
Sequence 14, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                               61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                       236 KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                                                   176 PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD 235
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                                         Gaps
                                                                               1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                       EKTISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK
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  Length 472;
                                         Indels
85.3%; Score 2146; DB 4;
85.1%; Pred. No. 1.4e-152;
tive 26; Mismatches 37;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 19PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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650/952-9881
  Query Match 85.39
Best Local Similarity 85.19
Matches 404; Conservative
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
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Patent No. 594511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                       84.5%; Score 2126; DB 2; Length 451; 87.8%; Pred. No. 4e-151; Live 23; Mismatches 30; Indels
                                                                                                                             Score All No. 4e-151;
Pred. No. 4e-151;
Annes 30;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 1nch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
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03-Jul-1997
N: 530
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NAME: SYODOGA, Craig G.
RECISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                 LENGIH: 451 amino acids
TYPE: Amino Acid
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Matches 397; Conservative
SEQUENCE CHARACTERISTICS
                                               ; TOPOLOGY: Linear
US-08-887-3528-14
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180 SSGLYSLSSVVTVPSSSLGTQTYICHVHHIFFSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239
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                                                                                                                                                                                                 Length 451;
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                                                                                                                                                                                               84.5%; Score 2126; DB 2;
87.8%; Pred. No. 4e-151;
iive 23; Mismatches 30;
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
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STATE: Californ's
: 650/225-1489
650/952-9881
                                                                                                                                                                                                                    Best Local Similarity 87.8
Matches 397; Conservative
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                                                                                                                      Linear
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US-08-887-352B-16
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Gaps

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20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQGLEWMGEIDPSDSYTN 78
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                                                                                                                                                                       : LOCATION: 1-451
: OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14
                                                                                                                                                                                                                                                                                             30; Indels
                                                                                                                                                                                                                                                                DB 4;
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 14, 2002, 15:17:06
Job time: 689 sec
                                                                                                                                                                     NAME/KEY: Artificial LOCATION: 1-451
                                                                                                                            TYPE: PRT ORGANISM: Artificial
                                                                                              SEQ ID NO 14
LENGTH: 451
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
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87.8%; Pred. No. 4e-151;
iive 23; Mismatches 3
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                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09109207C Patent No. 617213 GENERAL INFORMATION: EAPLICANT: Henry B. Lowman, Leonard TITLE OF INVENTION: Improved Anti-ig
                            FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
                                                                                                                                                                                                                               NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                            15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 451 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 87.8
397; Conservative
                                                                                                                                                                                                                                                                                                          650/952-9881
PRIOR APPLICATION DATA:
                                                            FILING DATE:
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US-09-109-207C-14
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TOPOLOGY:
US-08-466-151-65
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Best Local S
Matches 397,
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4.5
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2000
                                                         - protein search, using sw model
                                                        OM protein
                                                                                   Run on:
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August 14, 2002, 15:19:00 ; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

1 MGWSCIILFLVATATGVHSQ.......MHEALHNHYTQKSLSLSPGK 470 BLOSUM62DX Gapop 10.0 , Gapext 0.5 US-09-499-662-145 Perfect score: Sequence: Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

length: 0 length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_71:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scri	chain	Ig gamma-3 chain C Ig gamma-2a chain			gamma - 2b	heavy cha	gamma-1 chai	Ig heavy chain V r monoclonal antihod	gamma 2a			ភ	gamma		gamma 3	gamma-	heavy ch		gamma-1					
SUMMARIES	GHHU A23511	A60764 S37483	G2HU G4HU	G2MS11 S40295	S01321	S22080	S31459	S69339 PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	GIMS	PS0018	G1MSM	G3MSM
DB	42	0 0		Ч С	1 (2)	7	~	N (	~	7	4	~	7	Н	~	٦,	~	П	7	~	-	~	Н	Н
Length	330	377 469	326 327	474	475	470	472	3/4	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
% Query Match	69.8		64.0 63.5	61.5	59.7		58.4		50.3	50.1	49.8	49.5	49.1	48.9		48.1	•	•	•	٠	45.5	•	45.3	45.3
Score	1639.5	1637.5 1611.5	1610 1599.5	1547	1502.5	1476	1469	1434 1428.5	1267	1261	1253	1245	_	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	1144.5	1140	1139
Result No.	177	w 4	യ വ	r &	0	10	11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A; Molecule type: protein A; Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',2 A; Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',2 A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R; Ponstingl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A; Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Ni

A; Accession: A90564

Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain vHI	Ig Y heavy chain (
G2MSA	S00847	G2MSAB	G2MSAM	PS0019	S06611	G2MSBM	147162	S38864	S14683	S04845	869131	S38950	A49444	S69340	B46529
н	7	7	~	~	7	Н	~	~	~	~	~	7	N	~	CI
330	329	335	399	322	327	405	277	548	627	549	241	246	220	249	572
44.9	44.8	44.8	44.7	44.3	43.4	42.9	42.5	39.7	37.5	36.8	34.4	33,8	31.7	30.4	30.3
1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	866	945	927.5	866.5	852	797	764.5	761.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Cross-references: EMBL:217370
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A; Note: Lys-330 is removed after translation
B; Harris, L.J.
Submitted to the EMBL Data Library, October 1992
A; Reference number: $33904
A; Recession: $36861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 2-330 <HARN-
A; Cross-references: EMBL: 217370
A; Cross-references: EMBL: 217370
Cell 29, 671-679, 1982
A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of A; Reference number: S33887; MUID: 83001943
A; Accession: S33887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;235-330 <TAK>
A; Cross-references: EMBL:217370
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seg
A; Reference number: A90563; MUID:71064024
A; Contents: myeloma protein Eu
A; Accession: B90563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-96, R', 98-135 < CUN>
A; Note: this sequence has the G1m(3) marker, 97-Arg
R; Rutishauser, U; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A; Reference number: A90564; MUID:71064025
                                    C'Species: Homo saplens (man)
C'Species: Homo saplens (man)
C'Jaccession: A93431; Saguance_revision 18-Aug-1982 #text_change 16-Jul-1999
C'Jaccession: A93433; Saguance_revision 18-Aug-1982 #text_change 16-Jul-1999
C'Jaccession: A93433; A982; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A'Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A'Reference number: A93433; MUID:82274238
gamma-1 chain C region - human
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-330 <ELL>
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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Fitle: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c5, u) with an IGHG4 conv
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
                                                                                                      Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Fitle: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an 3
A;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DTPPPCPRCPEPKSCDIPPPCPRCPEPKSCDIPPPCPRCPAPELLGGPSVFLFPPRFDKDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNOVSLTCLVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: GDB:1GHG3
A,Cross-references: GDB:119339; OMIM:147120
A,Map position: 14q32.33-14q32.33
A,Introns: 94.33:115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin homology < IMM>
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A;Status: preliminary
A;Molecule Appe: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Best Local Similarity
Matches 312; Conserv
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G:Genetics:
A:Contents: annotation; disulfide bonds
G:Genetics:
A:Gene: GDB:120085; OMIN:147100
A:Cross-references: GDB:120085; OMIN:147100
A:Map position: 14932.33
A:Map position: 
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A91723
A; Accession: A91723
A; Accession: A91723
A; Molecule type: protein
B; Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Contents: annotation; Aisulfide bonds
A; Contents: annotation; Aisulfide bonds
A; Contents: annotation; A; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Ruse of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID: 77070267
                                                                                                                                   A; Molecule type: protein
A; Residues: 1-34, Q', 36-96, KK, 98-115, Q', 117-197, D', 199-238, D', 240, L', 242-268, E',
A; Residues: 1-34, Q', 36-96, KK, 98-115, Q', 117-197, D', 199-238, D', 240, L', 242-268, E',
Chote: this sequence has the Glm(17) and Glm(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hischmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Prinamestruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 R
A; Title: Die Prinamestruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 R
A; Contents: myeloma protein KOL; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 4.5e-93;
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                             A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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igen Primaerstruktur
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Ig gamma-2a chain - mouse
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C;Specials: Max musculus (house mouse)
C;Specials: Max musculus (house mouse)
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Reference number: S37483
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 cDUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region: immunoglobulin homology
C;Reywords: immunoglobulin homology <IMM>
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                                                                                                                                       Length 377;
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                                                                                                                                                                                                         11;
                                                                                                                                    Score 1637.5; DB 2
Pred. No. 3.7e-86;
7; Mismatches 11;
C;Keywords: immunoglobulin F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                       65.1%;
82.8%;
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Best Local Similarity 82.8
Matches 312; Conservative
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Best Local S:
Matches 304,
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A; Molecule type: DNA
A; Residues: 1-326 < CELL>
A; Residues: 1-326 < CELL>
A; Coss. references: GB: V00554; GB: J00230; NID: g32759; PIDN: CAB58438.1; PID: g6066056
A; Note: Lys-326 is probably removed posttranslationally
A; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A; Reference number: A92809; MUID: 81007873
A; Accession: A92809
A; Accession: A92809
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A; Residues: 1-24, F., 75, 75-57, EV, 60-85;132-171, 222',175, 'B',177-193, 'D',195-196, 'Q', I A; Residues: 1-24, F., 75-56-57, EV, 60-85;132-171, 222',175, 'B',177-193, 'D', 195-196, 'Q', I A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.W.
Mol. Immunol. 16, 923-925, 1979
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobul.
A; Reference number: A93132; MUID:80114419
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60-Ala and in the amid
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A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Rote: Trp-156 is at or near the complement-binding site
A; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of Reference number: A90752; MUID: 80001357
A; Roteents: myeloma protein Zie
A; Accession: A90752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
R;Ellison, J: Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy of A;Reference number: A93906; MUID:82197621
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;ritle: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;reference number: A90253; MUID:72033500
A;contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
                                                                                                                                                                                                                                                                                                                                                                                          KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                         NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                            ISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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A,Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revision
A;Note: the revised sequence differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-2 chain C region - human
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A;Accession: A93132
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OMIM: 147130

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A; Cross-references: GDB:119340;
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                                                                                                                                                         A.Map position: 1493.33-14932.33 c.complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap than district that it some cases, such as 194 and 194, the subunits associate into la C; Complex: An immunoglobulin cases, such as 194 and 194, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology city. The 0-82/Domain: immunoglobulin homology city.
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A; MCGCUIE type: DNA
A; MCGCIII type: DNA
A; MCGCIII the sequence was determined from the germline gene
B; MCGCIII the sequence was determined from the germline gene
B; MCGCIII the sequence was determined from the germline gene
B; MCGCIII the sequence managery S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
B; MCGCIII managerii managerii sequence of the constant
A; MCGCIII A90249; MUID: 70207560
A; Accession: A90249
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C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 1
C; Date: 02-By 1982 #sequence_revision 02-Apr-1982 #text_change 1
C; Accession: A90933; A90249; A02150
R; Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A; Title: Nuclectide sequence of a human immunoglobulin C-gamma4 characterice number: A90933; MuID:83157104
                    G.
                  A;Title: Structural studies of immunoglobulin A;Reference number: A93157; MUID:69064124 A;Contents: annotation; Sa, disulfide bonds
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                                                                                                                                            A; Cross-references: GDB:119338; OMIM:147110
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A; Residues: 1-30;81-326 <PIN>
C; Genetics:
               A; Title: Structural studies A; Reference number: A93157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 303; Conserv
                                                                                                                    A; Gene: GDB: IGHG2
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                                                                                          C;Genetics
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Use gramma-2b chain - mouse
C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1980 #sequence_revision 01-Dec-2000
C; Accession: S25057; A02157; A26232; A26233; A55598
R; Fischer, R; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A; Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi A; Reference number: S25057
A; Reference number: S25057
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-74 <FIS>
A; Cross-references: EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827
R; Yamawaki: Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A; Title: Complete nuclectide sequence of immunoglobulin gamma2b chain gene cloned from A; Reference number: A02157; MUID:80120716
A; Contents: a allele
A; Contents: a allele
A; Contents: a allele
A; Contents: a allele
A; Cross-references: GB:J00461
A; Residues: 138-161, 'L', 163-189, 'FP', 193-474 < YAM>
A; Residues: BNA; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
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                                                                                                                    141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                        .,
,
   327;
   Length
                                                             Indels
Score 1599.5; DB 1;
Pred. No. 4.5e-84;
9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%;
91.8%;
   Query Match 63.5
Best Local Similarity 91.8
Matches 303; Conservative
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S

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Iggamma-2a chain (mAb735) - mouse

G;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C;Accession: $40295

R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

submitted to the EMBL Data Library, January 1993

A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A;Reference number: $40295

A;Accession: $40295

A;Residues: 1-446 <KLE>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
C;Superfamily: immunoglobulin c region cypoprotein; immunoglobulin; pyroglutamic acid
E;1-446/Product: Ig gamma-2a chain #status experimental cMAT>
F;1-117/Domain: V-D-J region cVHD>
F;118-446/Domain: C region cCHH>
F;118-214/Domain: C1 region cCH1>
F;231-340/Domain: C2 region cCH2>
F;341-446/Domain: C3 region cCH2>
F;360-427/Domain: Immunoglobulin homology cIMM>
F;175-256,144-199,2561-321,367-4257Disulfide bonds: #status predicted
F;224-227,229/Disulfide bonds: interchain (to lain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;224,227,229/Disulfide bonds: interchain #status experimental
                                                                                413
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                                                                                                                PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
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6
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Best Local 8
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Acknowness HWC 14
Acknowness 10: 18.2535
Acknowness 13: 18.172, Pp. 174-189, FPP, 193-376, TT, 378-474 (TUI)
Acknowness 10: 18-172, Pp. 174-189, FPP, 193-376, TT, 378-474 (TUI)
Acknowness 10: 18-172, Pp. 174-189, FPP, 193-376, TT, 378-474 (TUI)
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Acknowness 10: 18-172, Pp. 174-189, FPP, 193-300, FR, 302-331, Acknowness 10: 18-18
Acknowness 10: 18-
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  regions of the murine gamma2b
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  untranslated
A; Title: Structure of the constant and 3' A; Reference number: A26235; MUID:80081501
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Matches 292; Conservative
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Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A;Reference number: S01320; MUID:88329081
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                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
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N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
4;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                     414
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A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Cross.1-475 CDEL3
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Mismatches
                                                                                                                                      438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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gamma 1 and
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C; Accession: S22080; S06610; A31303
R; Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A; Reference number: S22080
A; Reference number: S22080
A; Residues: 1-470 <SAN>
A; Robit : S06610; MUID: 90097956
A; Reference number: S06610; MUID: 90097956
A; Reference number: S06610; MUID: 90097956
A; Residues: 142-470 <SEN>
A; Residues: 142-470 <SEN>
A; Residues: 142-470
A; Residues: 38/1; 111/1; 221/1
C; Superfamily: immunoglobulin C region; immunoglobulin; membrane protein F; 161-225/Domain: immunoglobulin homology <IMM>
F; 318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iggamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 03-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31458
E;Patri, S; Nau, F.
Submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%; Score 1476; DB 2; 60.4%; Pred. No. 7.2e-77;
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Ly neavy chain, vieybou precursor numman
C; Species: Homo saplens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Date: 10-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: 65939; S7-664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Blochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: 569339; MUID: 95262687
A; Status: prellminary
A; Molecule type: mRNA
A; References: EMBL: X81695
R; Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A; Status: prellminary
A; Molecule type: mRNA
A; Reference number: 572664
A; Accession: 572664
A; Status: prellminary
A; Status: prellminary
A; Status: prellminary
A; Status: prellminary
A; Cross-references: EMBL: X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
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                                                                                                                                                                                                                                                                                                              TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 TIPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PATP >
A;Cross-rences: EMEL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                             114; Indels
                                                                                                                                                                                              tch 58.4%; Score 1469; DB 2; al Similarity 59.6%; Pred. No. 1.8e-76; 283; Conservative 66; Mismatches 114;
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Best Local Si
Matches 283;
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 04-F8b-1908 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C; Accession: PC4436
R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp A; Reference number: JC5810; MUID:98063277
A; Molecule type: protein
A; Molecule 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 181
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                                                                                                                                                                                                                                      65 ALEWLALIFWDDD-KRYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGY
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                                                                                                                                                                                  5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMOWVKQAPGO
                                                                                                                                                                                                                                                                                                                                                                63 GLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARN-RDY
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    Score 1434; DB 2;
Pred. No. 1.4e-74;
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Pred. No. 3.4e-74;
9; Mismatches 94
                                                                                         Mismatches
              56.8%; Sco. 58.0%; Pre-
tive 79;
    57.0%;
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Ig gamma 2b chain constant region - pig (fragment)
C; Species: Sus scrofa domestic (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147160
B; Kacskovics, I:, Sun, J:, Butler, J.E.
A; Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147158; MUID: 95015845
A; Ratus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Rocs references: EMBL: U03780; NID: 9433125; PIDN: AAA52218.1; PID: 9433126
C; Genetics:
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R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147158; MUID: 95015845
A; Accession: 147159
A; Actus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-328 <KAC>
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7
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                     373
                                                                                                                                                                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
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                                                                   254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
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C;Genetics:
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                   PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                      288 PREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYT
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                  Query Match 50.1%; Score 1261; DB 2; Best Local Similarity 69.6%; Pred. No. 8e-65; Matches 231; Conservative 41; Mismatches 54;
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HV12_MOUSE
HV13_MOUSE
HV03_MOUSE
HV03_MOUSE
HV1C_HUMAN
MUC_MOUSE
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Compugen Ltd.
       GenCore version
Copyright (c) 1993 - 2000
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                                   protein search, using sw model
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## ALIGNMENTS

Scoring table:	BLOSUM62DX Gapop 10.0		Gapext 0.5			ALIGNMENTS
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Total number of		isfying	hits satisfying chosen parameters:	105224	A P	
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Post-processing		Match Match first	0% 100% 45 summaries		OS OC	Ig gamma-1 chain C region. IGHG1. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Database :	SwissP:	SwissProt_40:*			o o a	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. VEB_TaxID=9606;
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	di		SUMMARIES		Z Z	"The nucleotide sequence of a numan immunoglobulin C gammai gene."; Nucleic Acids Res. 10:4071-4079(1982).
Result No. Score	Query Match Length	ength DB	B ID	Description	R R R	12) SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). MEDILNE-71064024; PubMed-5499771;
•	:	330 1	1 GC1 HIMAN	polasz company	RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.T. Edelman G.M.:
	64	326 1	1 GC2_HUMAN	. 0	RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
				P01801 MONIO Sapien P01870 oryctolagus	R. R.	u sequence chemistry 9
			1 GC2_CAVPO	P01862 cavia porce	RN	[3] CENTENTE OF 126-220 /FILL
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			1 GC3_MOUSE 1 GC1 MOUSE	P22436 mus musculu P01868 mus musculu	RA RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., Edelman G.M.;
				- 0	R	
12 1139	45.3	398	1 GC3M_MOUSE	PO1869 mus musculu PO3987 mus musculu	R R	acid sequence of neavy-chain cyanogen bromide fragments H5-H/; Biochemistry 9:31/1-3181(1970).
				P01863 mus musculu P20762 rattus norv	RN RP	[4] SEOUENCE (MYELOMA PROTEIN NIE).
				4 mus	RX.	MEDLINE-77070269; PubMed-826475;
				P01003 Mus Musculu P20760 rattus norv	R K	Fonstings h., hischmann w.; "The rule of antibody structure. The primary structure of a
			1 GCB_MOUSE	P01866 mus musculu	R	monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
Ŋ				1 mus	Z Z	peptides and discussion of the complete structure.";
			1 HV06_MOUSE	P01750 mus musculu P01755 mis misculii	RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
,	20.7			snum 0	RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
			-	POI/49 mus musculu PO1746 mus musculu	¥ \$	MEDLINE=83289131; PubMed=6884994; Schmidt W.E., Jung HD., Palm W., Hilschmann N.;
				3 mus	RT	"Three-dimensional structure determination of antibodies. Primary
				PO1/48 mus musculu P01855 rattus norv	RL	structure of crystailized Monoctonal immunogiobulin iger Nob, 1. ; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
29 486 30 486	19.3 19.3		1 HV49_MOUSE 1 EPC_HUMAN	P06328 mus musculu P01854 homo sapien	RN	[6] DISULFIDE BONDS.
					RX	MEDLINE=71064027; PubMed=4923144;
33 477		117 1	1 HV1G_HUMAN	FOL/34 mus musculu P23083 homo sapien	RT	Gall W.E., Edelman G.M., "The covalent structure of a human gamma G-immunoglobulin. X.

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                                                                                                                                                                                                                                               Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.6-A resolution.";

Biochemistry 20:2361-2370(1981).

"INSCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKER & THE GIM (NON-1) MARKERS.

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                                                                    MEDLINE-77070267; PubMed-1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
I'Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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InterPro; IPR003597; Ig_cd.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SWART; SW00410; IG_like; 1.
SWART; SW00407; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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MEDLINE-81208100; Pubmed-7236608;
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                  iochemistry 9:3188-3196(1970).
   Intrachain disulfide bonds.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL)
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MEDI.INE-82197621; PubMed-6804948;
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S -> A (IN MYELOMA PROTEINS TIL & 21E).
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8310878C6878CF9C CRC64;
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91.8%; Pred. No. 1.8e-103;
ive 10; Mismatches 13;
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                                                                                                                                         MEDLINE-70207566; PubMed-4192699;
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"Human immunoglobulin subclasses. Partial amino acid sequence of the Constant region of a gamma 4 chain.";
Blochem. J. 117:33-47(1970).
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     MEDLINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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Pred. No. 9.5e-103;
9; Mismatches 15;
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PIR; A02150; G4HU.
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35940 MW;
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InterPro; IPR003597; Ig_Cl.
InterPro; IPR003600; Ig_like.
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91.8%;
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SMART: SM00410; IG_like; 1.
SWART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                    SEQUENCE OF 1-30 AND 81-326.
         Ig gamma-4 chain C region
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                           Homo sapiens (Human).
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327 AA;
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                                                                                                                  DNA 1:11-18(1981).
                                                         NCBI_TaxID=9606;
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                                                                        MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
                                                                                                            Pratt D.M., Mole L.E.; "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Biochem. J. 151:37-349(1975).
STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
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Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 196: isolation of a cDNA encoding theavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA.
                                                                                                                                                                                                             441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                 MEDLINE=70110015; PubMed-5461106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-84030930; PubMed-6313520;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 01, Created)
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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SEQUENCE OF 1-128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSSVVSVTSSS---QPVTCNVAHPAINTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 263
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                                                                                                                     T -> M (IN D11 MARKER).

-> A (IN E15 MARKER).

-> E (IN REF. 2).

-> E (IN REF. 3).

-> E (IN REF. 3).

-> D (IN REF. 5).

-> E (IN REF. 5).

-> D (IN REF. 5).

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                                                                                Submitted (APR-1975) to the PIR data bank.
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SEQUENCE OF 4-68.
MEDLINE-71058471; PubMed-5538606;
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                 Pfam; PF00047; 19; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
IPR003597; Ig_cl.
047: iq; 3.
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Best Local Similarity 70.0°
Matches 229; Conservative
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323 AA;
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### INCECTION OF STRAIN OF
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Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
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the carboxyl-terminal
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Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-75036072; Pubmed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 227-311.
MEDLINE=75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
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Pred. No. 4.4e-76;
30; Mismatches 62; Indels
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                                                                                                                                                                                                                                                                                                                           Turner K.J., Cebra J.J.;

"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                                                                                                            [3]
SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; Pubmed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 13:4796-4803(1974)
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-:- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
                                                        REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 435
                                                                   MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264 (1982).
-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE RECION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-3 HEAVY CHAINS.

MISCELLANBOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM MISCELLANBOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM MISCELLANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                  Frangione B., Rosenwasser E., Prelli F., Franklin B.C.; "Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Biochemistry 19:4304-4308(1980).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-82247835; PubMed-6808505; Medsander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Steinmetz M., Barritault D., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human igG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-77021516; PubMed-823945;
Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
"The amino acid sequence of 'heavy chain disease' protein 2UC.
Structure of the Fragment of immunoglobulin G3.";
Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC)
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                                                                                                           DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-81021548; PubMed-6774747;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (DISEASE PROTEIN WIS)
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P01860;
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DOMAIN 12 73 HINGE.
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S -> N (IN OMM).
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/FTId=VAR_003891.
F -> Y (IN OMM).
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T -> A (IN OMM).
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11; Mismatches
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F -> Y (IN
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                                                                                                                                          EMBL; J00231; AAA52805.1; ALT_SEQ.
PIR; A02149; G3HUWI.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                             Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1.
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MIM; 147120; -
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
PIR: PS0017: PS0017.
PISSP: P01842; 7FAB.
InterPro: IPR003509; Ig_MHC.
InterPro: IPR003597; Ig_Cl.
Pfam: PF00047; Ig. 3.
SMART: SM004407; IG_HHC; 1.
                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JU-1999 (Rel. 38, Last annotation update)
19 gamma-1 chain region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                            region; Glycoprotein.
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63.4%; Pred. No. 2.8e-72;
tive 52; Mismatches 60;
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      Immunoglobulin domain; Immunoglobulin C

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                           329 AA
438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Mus musculus (Mouse).
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PIR; B02156; G3MSC.
HASSP; POL1857; 1FC1.
INTERPRO; 1PR003006; Ig_MHC.
INTERPRO; 1PR003597; Ig_C1.
INTERPRO; 1PR003597; Ig_C1.
INTERPRO; 1PR003500; Ig_like.
Ffan; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
IMMUNOGIODUIJIN GOMBIN; IMMUNOGIODUIJIN C:
ITANSMEMDYANG; ALTENATIVE SPLICING.
                            294 EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK
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HINGE.
CH2.
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Best Local Similarity 65.0%;
Matches 215; Conservative 44
                                                                                                                                                                                           STANDARD;
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P22436;
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GlycoSuiteDB; P01868; -.
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380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDIATRE-80205559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
             SEQUENCE FROM N.A.
MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musincel_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The disulphide bridges of a mouse immunoglobulin G1 protein."; Biochem. J. 126:837-850(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evolution of immunoglobulin subclasses. Primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21). MEDILINES-80012837; Pubmed-113776; ROGETS J., Clarke P., Salser W.; Sequence analysis of cloned cDNA encoding part of an i
                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
49 gamma-1 chain C region.
Mus musculus (Mouse).
                                                                                                                                              324 AA.
                                                                299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                  440 WOOGNVFSCSVMHEALHNHYTOKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy chain.";
Nucleic Acids Res. 6:3305-3321(1979).
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J. Biol. Chem. 253:6068-6075(1978).
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MEDLINE-78242288; PubMed-98524;
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MEDLINE-73008889; PubMed=5073237;
Svasti J., Milstein C.;
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24175.1; --
EMBL; V00793; CAA24176.1; --
PIR; A02159; GAA2
HSSP; P01842; 7FAB.
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                        gamma 1 chain gene.";
Cell 18:559-568(1979)
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P01868;
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Ig gamma-2B chain c reyrow.
Rattus norvegicus (Rat).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
MGD; MGI:96446; Igh.4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR0047; ig_al.
SWART; SW00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                    CHAIN).
CHAIN).
                                                                                                                                                                                                                                  LIGHT CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
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N -> D (IN REF. 3).

N -> D (IN REF. 3).

N 3338812F301F2C93 CRC64;
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INTERCHAIN (WITH A H
INTERCHAIN (WITH A H
INTERCHAIN (WITH A H
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ilarity 62.3%; Pred. No. 1.3e-71;
Conservative 55; Mismatches 60;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
1G gamma-2B chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 AA.
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SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed-3149946;
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276
278
35704 M
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                                                                                                                  Alternative splicing
                                                                                                                                                                                                                                                                                                                                                              324
276
278
324 AA;
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les 207; Conserv
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138
174
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Best Local Si
Matches 207;
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DOMAIN
DISULFID
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CONFLICT
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P20761;
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Cell 18:559-568(1979).
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                                                            domain.
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3;
      "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
PIR; PS0018; PS0018.
                                                                                                                                                                                                                                                        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                     PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                                                                                                                                                       REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
                                                                                                                                                                                                                                                                                                                                                                          201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS-----CDKTHTCPPCPA 254
                                                                                                                                                                                                                                                                                                                                                                                                   375 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 434
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                 MEDLINE-80045036; PubMed=115593; DubMod=115593; Memolo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                        6
                                                                                                                                       INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                      DB 1; Length 333;
                                                                                                                       INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                  -/L;
68; Indels
                                                                                                                                                                                           55F8B64D48D460A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
                                                                                                     Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                   45.5%; Score 1144.5; DB 63.7%; Pred. No. 1.5e-71.1ve 45; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                      VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                393 AA.
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                             HSSP, P01842; 7FAB.

InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_cl.
InterPro: IPR003600; Ig_lke.
Pfam: PF00047; Ig; 3:
SMART: SM00410; IG_lke; 1.
SMART: SM00407; IGC, 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                           36497 MW;
                                                                                                                                                                                                                                      Matches 214; Conservative
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80
106
1109
1112
207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse)
                                                                                                                                                                        147
253
333 AA;
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                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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ID GCIM_MOUSE
AC P01869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALFERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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SEQUENCE OF 323-393 FROM N.A. MEDLINE-82197626; PubMed-6804950; Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O. "mRNA for Surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 10;
                                                                                                                                                                                                                SEQUENCE OF 323-366 FROM N.A. MEDIATE-8115295; PubMed-6799207; MEDIATE-82115295; PubMed-6799207; Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN).
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4CC88343B7A1CE27 CRC64;
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Pred. No. 3.7e-71;
5; Mismatches 60;
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CH2.
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MEDLINE=82222190; PubMed=6283537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.3%; Sco
62.2%; Pre
tive 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01842; 7FAB.
MGD; MGI:99446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
Pfam; PP00047; ig; 3.
SMART; SM00407; IGC1; 2.
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Matches 206; Conservative
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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                       ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                               173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYIPPPPK 232
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                                                                                                                                   319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                           "The structure of the mouse immunoglobulin in gamma 3 membrane gene
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SEQUENCE FROM N.A.
MEDLINE-85027161; Pubwed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma - 3 chain C region, membrane-bound form.
Mus musculus (Mouse).
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
INCEPPO; IPR003006; Ig_MHC.
INTERPO; IPR003597; Ig_C1.
INTERPO; IPR003507; Ig_C1.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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P03987;
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MEDLINE=81198976; PubMed=6262729; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.", Nucleic Acids Res. 9:1365-1381(1981).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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64.7%; Pred. No. 4.5e-71;
11ve 44; Mismatches 68;
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21-JUL-1986 (Rel. 01, Last sequence update)
19-VMX-2000 (Rel. 39, Last annotation update)
1g gamma-2A chain C region, A allele.
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HINGE.
Alternative splicing
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MEDLINE=81076554; Pubmed-6777755;
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398 AA;
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Matches 213; Conserv
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SEQUENCE FROM N.A.
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EEMTKNOVSLITCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKS 438
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MEDLINE-81223894; PubMed-6787604; ollo R., Auffray C., Morchamps C., Rougeon F.; comparison of mouse immunoqlobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
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                                                                                                    Bourgols A., Fougereau M., Rocca Serra J.; "Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid Sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function."; Eur. J. Biochem. 43:423-435(1974).
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B84361C5445A6864 CRC64;
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                                                          Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
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MEDLINE=74175517; PubMed-4831970;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
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Sciurognathi; Muridae; Murinae; Rattus.
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Eur. J. Immunol. 18:317-319(1988).
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        Immunoglobulin domain;
        Immunoglobulin c region.

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15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C region.
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                                                                                                                                                                              RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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MEDLINE-88166903; Pubmed-3127222;
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HSSP; P01857; 1FC1.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR0035097; Ig_C1.
InterPro: IPR0035097; Ig_C1.
Efam; PF00047; Ig; 3.
SWART; $M00410; IG_Like; 1.
SWART; $M004107; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X07189; CAA30169.1; -.
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                               377
                                                                                                                                                                                                                                           REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                                              LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-2A chain C region, B allele.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                     MEDLINE-87BL/6;
MEDLINE-82037861; PubMed=6170065;
SCHWEIL B., Baltimore D.;
Schweil A.L.M., Mueller-Hill B., Baltimore D.;
Mulliple differences between the nucleic acid sequences of the
1962aa and 1962ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                 297 DSWARGDIYTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                                                                                                                                                                                                                                              SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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SEQUENCE.
MEDLINE=82037777; PubMed=6794027;
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InterPro: IPR003597; Ig_cl.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
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SEQUENCE FROM N.A.
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                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK----SCDKTHTCPPCPA
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  Mismatches
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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sp\_plant:\*
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SUMMARIES

		Description	Q9d814 mus musculu	O991c4 mus musculu	mus	Q99131 mus musculu	Q9rla4 mus musculu	Q91z05 mus musculu	Q95m34 equus cabal	Q96pq8 homo sapien	Q921k1 mus musculu	O96qa6 homo sapien	Q91wt3 mus musculu	Q9brv0 homo sapien	Q91wt1 mus musculu		096bb9 homo sapien	рошо
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		Match Length DB	473	463	473	468	437	473	337	701	278	614	481	200	481	488	597	496
ф	Query	Match	65.1	64.6	63.0	62.1	57.0	56.5	50.2	49.9	39.1	36.9	35.3	34.0	33.2	32.5	32.4	32.0
		Score	1637.5	1626.5	1586.5	1564	1435.5	1422.5	1263.5	1257	984	929.5	888.5	857	834.5	818	814.5	908
	Result	No.	1	2	ო	4	S	9	7	80	6	10	11	12	13	14	15	16

## ALIGNMENTS

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Gaps

Indels

Length 463;

DB 11;

9

us-09-499-662-145.rspt

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61 GQGLEWYGEIYPGSGNTYYSEKFKGKATLITDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 RDCG----CKPCICTVPEV---SSVFIEPPKFKDVLTITLTPKVTCVVVDISKDDPEVQF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
                                                                                                                                                                                                                                                                                                                                                                  1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003888; AAH03888.1; -. HSSP; P01842; 7FAB.
                 Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
BMART; SM00407; IG; 2.
SMART; SM00407; IGv; 1.
SMART; SM004107; IGv; 1.
SMART; SM004107; IG_Like; 1.
PROSITE; PS002909; IG_MHC; UNKNOWN_1.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                  64.6%; Score 1626.5; DB 11
63.6%; Pred. No. 1.5e-128;
ive 72; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR003599; Ig.
Interpro; IPR003599; Ig.Cl.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MRC.
Interpro; IPR003596; Ig_WV.
Pfam; PF00047; ig; 4.
SMART; SM004409; IG; 2.
InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.6
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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099L25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K - - - - - SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KITPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                  94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (REB-2001) to the EMBL/GenBank/DDBJ databases. Submitted (REB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC001842; ARM03435.1; -. InterPro; IPR003599; Ig... InterPro; IPR003597; Ig.cl. InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                           9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                  65.1%; Score 1637.5; DB 1:
63.7%; Pred. No. 1.9e-129;
                                                                                                                                                                                                                                                                                                                                                                                                               70; Mismatches
                 InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig_c1.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
PRam; PR00047; Ig; 4.
SWART; SW00409; IG; 2.
SWART; SW00410; IG_like; 1.
PROSITE; PS00290; IG yHC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
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099LC4;
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Thu Ang 15

96352328B3332ADB CRC64;

51661 MW;

468 AA;

SEQUENCE

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                                                                                                                                                                                         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                          121 --YSNN-WYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                            TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                                                                                             VEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                                                                                                               VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                      1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1586.5; DB 11; Length 473;
Pred. No. 3.7e-125;
61; Mismatches 106; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
SMART; SM00407; IGC1; 3.
SMART: SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus musculus (Mouse).
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01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro; IPR003599; Ig.
InterPro; IPR003599; Ig.cl.
InterPro; IPR003600; Ig_cl.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00407; IG_L; 3.
SMART; SM00406; IGC; 3.
SMART; SM00406; IGC; 3.
                                                                                      63.0%;
63.4%;
                                                                                                                 Conservative
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                                                                                                     Similarity
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                                                                                                               301;
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Best Local S
Matches 301
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Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;
"Cloning of cDNs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
rushied chain antibody (scrV)."
Usubmitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, Ar152372; AAD40243.1; -.
REMBL, AR152372; AAD40243.1; -.
RIGEPRO; IPR003606; Ig_HKe.
RIGEPRO; IPR003606; Ig_HKe.
RIGEPRO; IPR003566; Ig_V.
REPRO; PR00406; IG_X.
REPRO; ROWART; SM00406; IG_X; I.S.
REPROSTIE; PS00290; IG_HKC; UNKNOWN_1.
                                                                                                           GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                         YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                      181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                          Gaps
                                                     9
                                                                              9
                                                  241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                           01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMA1 HEATY CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Murinatis (Mouse).
McBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                  359 ISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                          ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 468;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5C3A7BB3EE7D697C CRC64;
Query Match 62.1%; Score 1564; DB 11; Best Local Similarity 63.1%; Pred. No. 2.8e-123; Matches 298; Conservative 60; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437
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Q9R1A4;
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                                                                                                                              60 DSVKGRETIYKDKDRNILSLQMSSLRSEDTAMYYCARG-DYS----AYWGPGTLVTVSA 113
                                                                                                                                                                    ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                   319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                Gaps
                                                       21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWWQWVKQAPGQGLEWMGEIDPSDSYTNYN 80
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                                                                                                                                                                                                                                                                                 259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
  DB 11; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 473;
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                              Indels
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SEOUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
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Q91205;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
                             96;
57.0%; Score 1435.5; DB 1
59.3%; Pred. No. 1.7e-112;
ive 71; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Submitted (JUL-2001) to the
EMBL; BC010327; AMH10327.1;
                             Conservative
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              Similarity
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 Query Match
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"Organization of the equine immunoglobulin heavy chain constant region genes. II. Alignment of c.mu, c.gamma, c.epsilon and c.alpha genes."; Immunobiology 199:105-119(1998).
EMBL: AJ300675; CAC44624.1; -.
                                                                     417
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254
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               :|:| |||||||:|| ||||::|| ||||||::|| ||::|| ||::|| SLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPI
                                                        KT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                 298 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                                                                                 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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Last sequence update)
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CHAIN CONSTANT REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wagner B., Overesch G., Sheoran A., Holmes
Leibold W., Radbruch A.;
                                                                                                                                                                                                                                                                                                                                        337
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Similarity 36.7%
12; Conservative
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Best Local Simil
Matches 212; C
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  Query Match
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Matches 186
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                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                   Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                     Hu Z., Garen A.; "Targeting tissue factor on tumor vascular endothelial cells ar cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 49.9%; Score 1257; DB 4; Length 701; al Similarity 99.1%; Pred. No. 3.5e-97; 230; Conservative 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC012207; AAH12207.1; -.
                                                                                                                                                                                                                                                                                                 58686.1; -. 77826 MW; 94AC6CEB42CC992F CRC64;
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                                                                                                                         096P06.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
                                                    LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                   701
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SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
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                                                                                                                                                                                             61 GOGLEWIGNINPNSGGTNYNEKFKNKATLAVDKSSSTVYMOLSSLTSEDSAVYYCTRGYG 120
                                                                                                                                                                                                                                                                                     YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GQALEMMGWITPFNGNTNYAQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCARG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YSNNW--YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 EKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD 357
                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                             GOGLEWMGEIDPSDSYTNYNOKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 614;
  Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. SEEF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CDKTHTCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:15420).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.9%; Score 929.5; DB 4;
36.7%; Pred. No. 1.1e-69;
ive 84; Mismatches 166;
Score 984; DB 11;
Pred. No. 8.8e-75;
; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 K----SCDKTHTCPPCPAPELLGGPSVFLFPPKPK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TKVDKRVEPKS---
  39.1%; Scc
67.1%; Pre
tive 33;
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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9

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Query Match
Best Local Similarity 40.9
Matches 205; Conservative
                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein
SEQUENCE 500 AA;
                                                                                                                                                                                             NCBI_TaxID=9606;
                     470
                                          463
                                   462 GK
                      469 GK
                                                                                             Q9BRV0
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                                                              475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                             ----VELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
           358 QDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                    PSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRWSCIILFLVATATGVNSQVQLQQPGAEIVRPGASVKLSCKTSGYTFTDYWMNWVKORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEKTISKAKGOPREPOVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGO---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                  35.3%; Score 888.5; DB 11; Length 481; 42.7%; Pred. No. 2.1e-66; 1ve 73; Mismatches 172; Indels 31;
                                                                                                                                                                                                                                                                                                                              TISSUE-COLON;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011488; AAH13488.1;
Hypothetical protein.
SEQUENCE 481 AA; 52022 MM; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                              091WT3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.0 KDA PROTEIN.
Mus musculus (Mouse).
                                                                                                                            431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                                                                  572
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                                                                                                                                        481
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                                                                                                                                                                                                     PRELIMINARY;
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Matches 206; Conserv
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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091WT3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYS---NNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK-------DTLM
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                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
HYMOTHETICAL 54.2 KDA PROTEIN.
Eukaryota; Metacao; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.0%; Score 857; DB 4; L
40.9%; Pred. No. 9.9e-64;
Live 69; Mismatches 177;
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SMART; SM00409; IG: 2.
SMART; SM00406; ICU; 1.
SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC005951; AAH05951.1; -...
HSSP; P01789; IMCP.
InterPro; IPR003599; Ig.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003606; Ig_MHC.
InterPro; IPR003606; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-PROSTATE;
Strausherg R.;
Submitted (APR-2001) to the EM
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; IMCP.
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18;

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Q91WR1;
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Q96BB9
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RESULT 14
Q91WR1
                      091WR1
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         FYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GGGWAFDYWGQGTTLTVSSEPAREPIIYPLT-FPQALSSDPVIIGCLIHDYFPSGTMNV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 NCPGICSPPTPPPPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                          091WT1 PRELIMINARY; PRT; 481 AA.
091WT1;
091WT1;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN.
MAS musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTW----EPSTGKDAVQKKAVQNSCGCXSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                  Length 481;
                                                                                                                                                                                                                                                                                                                                                                33.2%; Score 834.5; DB 11; Length 40.2%; Pred. No. 7.4e-62; Ive 73; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC013490; AAH13490.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                    1 protein.
481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                     450 VMHEALHNHYTQKSLSLSPGK 470
                                                                  Best_Local Similarity 40.29
Matches 194; Conservative
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=COLON;
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GK 463
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                            RESULT 13
Q91WT1
ID Q91WT1
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121 YSNNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNO-VSLTCLVKGFYPSDIAVEWESNG
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
14 POTHERIZAL 65.0 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 818; DB 11; Length 4; Pred. No. 1.8e-60; 85; Mismatches 177; Indels
                                                                                                                                                                                                                                                         TISSUE-KIDNEY,
Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013399; AAH13539.1; -.
Hypothetical protein.
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
                                                             Last sequence update)
Last annotation update)
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                                           Created)
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                                                                                                         HYPOTHETICAL 53.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      32.5%;
39.2%;
                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID=10090;
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Best Local Simi
Matches 191;
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16;

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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                        176 PVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 NKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 PDQDTAIRVFAIPPS-FASIFLIKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNI 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REBQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQYYT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61. GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARN-R 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 LPPSREEM1-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF 428
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                        231 N-----TKVDKRVEPKS------CDKTHTCP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCV
                                                                                                                                                                             Query Match 32.4%; Score 814.5; DB 4; Length 597; Best Local Similarity 32.6%; Pred. No. 4.8e-60; Matches 190; Conservative 94; Mismatches 179; Indels 119;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                           SEQUENCE FROM N.A.
TISSUE=PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO15760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Search completed: August 14, 2002, 15:22:18 Job time: 686 sec

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August 14, 2002, 15:15:38; search time 230.21 Seconds (without alignments) 226.770 Million cell updates/sec
                                                                                                                                                                                                               1 MGWSCIILFLVATATGVHSQ.......MHEALHNHYTQKSLSLSPGK 470
 4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   747574 segs, 111073796 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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2517
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length: 2000000000
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Perfect score:
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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981\_DAT:\*

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-embl/AA1982\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-embl/AA1985\_DAT:\*

SIDSI/gcgdata/hold-geneseqp-embl/AA1985\_DAT:\*

SIDSI/gcgdata/hold-geneseqp-embl/AA1985\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-embl/AA1986\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-embl/AA1989\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-embl/AA1999\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1991\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1991\_DAT:\*

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SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1991\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1995\_DAT:\*

SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1995\_DAT:\* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1997.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1999.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1999.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2000.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2001.DAT:\*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2001.DAT:\* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\* A\_Geneseq\_032802:\* 9: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Humanised anti-Fas Humanised HFF7A de Anti-Fas humanised Humanised anti-Fas Humanised HFF7A de Humanised HFF7A de Humanised HFF7A de Humanised anti-Fas Humanised anti-Fas Anti-Fas humanised Humanised anti-Fas Description SUMMARIES AAW83037 AAB14779 AAW90929 AAW83036 AAB14776 AAW90926 AAW90936 AAM52156 AAW90933 AAW90934 AAW90935 21 21 21 21 21 21 21 22 21 Query Match Length DB 1000 999 999 999 999 999 999 33 2517 2514 2512 2512 2511 2511 2511 2498 2498 2498 2498 2498 2498 Score Result . 9

(SANY ) SANKYO CO LTD.

2349.5 2344.5 2344.5 2344.5 2344.5 2344.5 2348.5 2338.5 2338.5 2293.7 2293.7 2284.9 2288.5 91.1 465.2 2288.5 91.1 465.2 2288.5 91.1 465.2 2288.5 91.1 465.2 2288.5 91.1 465.2 2288.5 91.1 465.2 2288.5 91.1 465.2 2288.8 91.7 466.2 2225.5 88.8 88.8 449.14 2225.5 88.8 88.8 449.14 2226.5 88.8 88.8 449.14 22203.5 88.7 2203.5 2203.5 88.7 2203.5 2203	HMFG-1	HMF.C-T	HMFG-1	HMFG	HMFG-	Heavy chain of hmA	Humanised 323/A3 (	Humanised 323/A3 (	A dimeric anti-CD2	Chimeric 2403 IgG	Monoclonal antibod	Sequence of antibo	Human reshaped F19	Completely humanis	Amino acid sequenc	Antibody D heavy c	Ganglioside GM2 an	Human immune syste	-	Humanised anti-IL-	Humanised anti-IL-	Chimeric mouse/hum	Anti-IL-8 humanise	Human type antihum	Amino acid sequenc		-	Anti-5T4 single ch	Amino acid sequenc	Human type antihum		D9D10 heavy chain	44	Donested Campage
2349.5 3 2344.5 4 23344.5 5 23344.5 6 2338.5 6 2338.5 7 3 3 3 3 7 4 6 5 6 6 6 8 6 9 7 8 6 6 9 7 8 6 6 9 9 7 8 6 6 9 9 7 8 6 9 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		AAM52158	AAM52161	AAM52157	AAM52160	AAW48650	AAB72228	AAB72232	AAB08026	AAE03755	AAW88464	AAR24442	AAY50166	AAR43339	AAW49816	AAR31023	AAB83156	AAB36210	AAY29458	AAB30322	AAY77766	AAY50157	AAW69316	AAG64475	AAB83838	AAU14177	AAG64471	AAW86003	AAG63640	AAG64469	AAG64473	AAW85689	AAW85692	AAR22757
2349.5 2344.5 2346.5	22	77	22	22	22	19	22	22	21	22	20	13	20	14	19	14	22	22	20	21	21	20	19	22	22	22	22	20	22	22	22	20	20	
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	93.3	73.T	93.1	92.9	92.9	91.7	91.1	6.06	90.7	90.7	89.7	9.68	89.4	88.8	88.8	88.7	88.5	87.6	87.5	87.5	87.5	87.5	87.2	87.1	87.0	87.0	86.9	6.98	86.8	86.8	86.5	86.4	86.4	86.0
11111111111111111111111111111111111111	34	34	34	33	2338.5	2307	σ	$\infty$	2284	2283	2258	S	2251	2235	2235	2233	2226.5	2205.5	2203.5	2203.5	2203.5	2203	2194.5	2191.5	2190	2189	2188.5	2187	2184.5	2183.5	2176.5	2174	2174	2165
	12	7	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosoclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple solerosis; Basedow's disease; thrombopenia purpure; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Humanised anti-Fas designed heavy chain Heu 3 protein. AAW90935 standard; Protein; 470 AA. 98JP-0276881. 98JP-0276882. 99EP-0307711 08-AUG-2000 (first entry) 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; EP990663-A2 05-APR-2000 Synthetic. AAW90935; AAW90935  361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

Takahashi T; Tamaki I, Nakahara K, Haruyama H, Serizawa N, 

WPI; 2000-258930/23. N-PSDB; AAA11646 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

2; Page 180-182; 263pp; English. Claim This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cells with an abnormal Fas/Fas capoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-antemic, antidabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rememacid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, cleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, antipher allergic anemia, sterility myasthenia gravis, antipher allergic anemia, antipher allergic and antipher allergic anemia, antipher allergic and antipher allergic anemia, antipher allergic and antipher and antipher allergic and antipher aller dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminanc, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mind the native ligand, do not induce liver disease, and have reduced risk of a humanised anti-rea antibody response. This sequence represents which is described in the method of the invention.

470 AA; Seguence

; 0 240 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 ggglewmgeidpsdsytnyngkfkgkatltvdtststaymelsslrsedtavyycarnrd 120 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 Gaps 9 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP ö Length 470; Indels 100.0%; Score 2517; DB 21; 100.0%; Pred. No. 1.7e-144; ive 0; Mismatches 0; 1 Query Match
Best Local Similarity 100.
Matches 470; Conservative 61 61 121 181 241 121 181 ò a δ 염 ò g ò g δ

Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimico disease; rheumatoid arthritis; graft versus host disease; sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Takahashi T; 421 ldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk 421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK Humanised anti-Fas designed heavy chain Heu 1 protein. Serizawa N, Haruyama H, Nakahara K, Tamaki I, AAW90933 standard; Protein; 470 AA. 99EP-0307711. 98JP-0276881. 98JP-0276882. 08-AUG-2000 (first entry) (SANY ) SANKYO CO LTD. 2000-258930/23. N-PSDB; AAA11644 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; EP990663-A2. 05-APR-2000 Synthetic. AAW90933; C4 AAW90933 RESULT ò g 

Interpretation describes a mover, instance, and proceed and proceded (1) that, induces a poptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between carti-anemic, antidiabetic, anti-allergic, anti-arthritic, anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antidiateribity, neuroprotective, antitrheumatic, nephrotropic, antidiateribity, neuroprotective, antitrheumatic, antidiate and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic constraints host disease, slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, solecterme, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopeania purpura insulin cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (1) selectively This invention describes a novel humanized anti-Fas antibody-like

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YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS

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KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV

420

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

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inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-nurihe antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu I which is described in the method of the invention.
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Pred. No. 2.6e-144;
1; Mismatches 0;
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EP990663-A2

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This invention describes a novel humanized anti-Fas antibody-like
molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
fas and its ligand. The products of the invention have anti-inflammatory,
cantidiabetic, anti-alergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertillity, neuroprotective,
cantidiaterioscierotic, cardiant and hepatropic activity. (1) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
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inhibition of ligand binding. (1) are used to treat and/or prevent
capoptosis by binding to cell surface Fas or inhibit it by competitive
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versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
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multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
cdisease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic, and transplant rejection. (1) selectively
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind and contindue liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
changed anti-Fas antibody heavy chain construct designated Heu 2
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Pred. No. 3.5e-144;
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99.6%;
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98JP-0276882
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30-SEP-1998;
                    05-APR-2000
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                                                     KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
                                                                                                                                                                                                      HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autofumune disease; Hashimoto's disease; systemic luque erythematosus; graft versus host disease; systemic luque erythematosus; graft versus host disease; soleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; attoriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                     LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                             Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
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/label- Sig_peptide
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/label= CDR_H3
/note= "claim 9"
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/label- Constant
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/label= cDR_H1
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/label= CDR_H2
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97JP-0082953
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01-APR-1997;
25-JUN-1997;
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This is the amino acid sequence of the HV type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. It includes humanising R4d6 and A76T amino acid substitutions that are includes humanising R4d6 and A76T amino acid substitutions that are are conserved in the human IGG heavy chain. Host Escherichia coli paper producing humanised HV type HFE7A heavy chain and DNA canciding humanised antibodies by culturing host cells. Humanised producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW8301-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease, scleroderma, Goodpasture syndrome, Crohn's disease, thermatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basadow's disease, thermatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basadow's disease, thermatoid arthritis, animula, hepatitis, albs and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                         proteins bind conserved epitope of Fas antigen - rugs in animal models and to treat Fas-associated Immune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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99.6%; Pred. No. 4e-144;
tive 2; Mismatches 0;
Tohru T;
                                                                                                                                                                                                                                                                                            Claim 22; Page 225-227; 292pp; English.
                                                                                                                                                                        used to evaluate drugs in animal m
diseases e.g. autoimmune disease,
myocarditis, hepatitis and AIDS
Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.8
Best Local Similarity 99.6
Matches 468; Conservative
Nobufusa S,
                                                       WPI; 1998-543440/47.
N-PSDB; AAV70080.
                                                                                                                                               antibodies and
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Masahiko O,
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99EP-0307711.
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98JP-0276882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, alleryy, atcpy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                 Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Iigand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                               Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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421 ldsdgsfflyskltvdksrwqggnvfscsvmhealhnhytqkslslspgk 470
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                                                                                                                            Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2511; DB 21;
Pred. No. 4e-144;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Page 108-109; 139pp; Japanese.
                                                        AAB14779 standard; Protein; 470 AA
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                                                                                                                                                                                                                                                                                                                                               98JP-0276883.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 468; Conservative
                                                                                                                                                                                                                                     Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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Best Local Similarity
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                                                                                                      24 - NOV - 2000
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                                                                                AAB14779;
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anti-allergic, anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosupressive; thyronimhetic; antirhematic; antirhemator, antirhertility; neuroprotective; antiarteriosclerotic; hepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatold arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
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                                                                                                        KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                360
                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic;
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                        KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised HFE7A designed heavy chain protein #2.
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capoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antivaral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antilnfertility, neuroprotective, antiarterisoclerotic, cardiant and hepatropic activity. (I) induce antiarterisoclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent of diseases associated with the Fas/Fas ligand system, especially systemic input serythematosus, Hashimoto disease, rheumatoid arthritis, graft or enemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatisis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEF7A designed heavy chain which is used in
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Sequence

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                                                                                                61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                           121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                              240
                                                                                                                                                                                                           241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                               YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                               361 KAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV 420
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                              WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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Score 2511; DB 21; Length 470;
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                       Indels
           Pred. No. 4e-144;
2; Mismatches 0;
99.88;
                        468; Conservative
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HFE7A, monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A, autolimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune heemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease;
                                                                                thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jun O, Kimihisa I; , Tohru T;
Anti-Fas humanised antibody HFE7A heavy chain.
                                                                                                                                                                   1..19
/label- Sig_peptide
20..470
/label- Mat_protein
                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akio S, Hideyuki H, Hiroko Y, Ju
Masahiko O, Nobufusa S, Shin Y,
                                                                                                                                                                                                        20..140
/label= Variable
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/label- Constant
                                                                                                                                                                                                                                                                 /note= "claim 9"
                                                                                                                                                                                                                                                                                            "claim 9"
                                                                                                                                                                                                                                                                                                                /label= CDR_H3
/note= "claim 9"
                                                                                                                                                                                                                                                                            69..84
/label= CDR_H2
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/label= CDR_H1
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                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                         SANY ) SANKYO CO LTD.
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998
                                                                                                                                           Synthetic.
                                                                                                                                                              Key
Peptide
                                                                                                                                                                                        Protein
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This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. colipgHSL7A62 SANK 73397 harbors plasmid gHSL7A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA encoding human IgGl constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to antibodies and proteins bind conserved epitope of Fas antigen - 1 to evaluate drugs in animal models and to treat Fas-associated bases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, Claim 22; Page 212-213; 292pp; English. used to evaluate drugs in animal m diseases e.g. autoimmune disease, myocarditis, hepatitis and AIDS WPI; 1998-543440/47. N-PSDB; AAV70079. Nev

AAW83036 standard; Protein; 470 AA

AAW83036

(first entry)

15-MAR-1999

AAW83036;

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Thu Aug

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                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, mayocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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                                                                                                                                                                                                    Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-Fas antibody heavy chain, SEQ ID NO:89
                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                 99.2%; Score 2498; DB 19; 99.1%; Pred. No. 2.5e-143; ive 2; Mismatches 2;
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                                                                                                                                                                                                                 al Similarity
466; Conserv
                                                                                                                                                     470 AA;
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Chimeric - E
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allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFE7A-derived anti-Fas antibodies.
                                                                                                                                                                                                                                       The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-Imman Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases,
                                                                                                                                                   for the diseases caused by an abnormality
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                                                                                                                                                                   the Fas/Fas ligand system e.g. autoimmune diseases, contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
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Pred. No. 2.5e-143;
; Mismatches 2;
                                                                                                                                                                                                               Claim 21; Page 95-96; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                   Preventive or treating agent
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99.1%;
                                           98JP-0276883.
              99JP-0278301.
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                                                                        (SANY ) SANKYO CO LID
                                                                                                      WPI; 2000-485645/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 AA;
                                                                                                                                                                                  anti-Fas antibody
                                                                                                                     N-PSDB; AAA72159
              30-SEP-1999;
                                           30-SEP-1998;
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Matches 466;
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AAW90926

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Length 470;

DB 21;

Score 2498; DB 21; Pred. No. 2.5e-143;

99.2%; 99.1%;

Similarity

Query Match Best Local S

standard; Protein; 470 AA. 

AAW90926;

(first entry) 08-AUG-2000

Humanised HFE7A designed heavy chain protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rhemmatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; albergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2

05-APR-2000

99EP-0307711 29-SEP-1999; 98JP-0276881 30-SEP-1998;

98JP-0276882 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Nakahara K, Tamaki I, Takahashi T; Serizawa N, Haruyama H,

WPI; 2000-258930/23. N-PSDB; AAA11597 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 15; Page 134-136; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
c apoptosis in cells with a normal system, by inhibiting binding between
apoptosis in cells with a normal system, by inhibiting binding between
c apoptosis in cells with a normal system, by inhibiting binding between
c anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antilnfertility, neuroprotective,
c antilntion of ligand binding. (I) are used to treat and/or prevent
c apoptosis by binding to cell surfaces or inhibit it by competities
c limibition of ligand binding. (I) are used to treat and/or prevent
c lupus erythematosus, Hashimoto disease, reminded previous or hypoplastic
c userias host disease, Soloreoferme, Cooleasture syndrome, Crohn's
c disease, addisease, Soloreoferme, Soloreoferme, Cooleasture, Addison's disease, thrombopenia purpura, insulin
c disease, addisent dishebetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
c (B, C or D) or alcoholic), and transplant rejectively induce it in abnormal
c ells. They bind to both human and murine Fas, so can be evaluated in
c murine disease models. (I) act on the active site of Fas, i.e. they minic
cells. They bind to both human and murine Fas, so can be evaluated in
c murine disease models. (I) act on the active site of Fas, i.e. they minic
cells. They human anti-murine antibody response. This sequence represents
c humanised anti-Fas antibody HEZAA des

AA; 470 Sequence

ö anti-allergic; anti-arthritic; anti-dimension, anti-dimension, anti-dimension, anti-dimension, anti-dimension, anti-dimension, anti-dimension, anti-dimension, anti-dimension, anti-fas; dermatological; immunosuppressive; thyromimetic; anti-frematic; anti-fas; hephrotropic; anti-farility; neuroprotective; anti-farilitosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabates mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. 300 360 61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 360 Gaps 361 kakggprepgvytlppsreemtkngvsltclvkgfypsdiavewesnggpennykttppv 420 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60 antibody; human; anti-inflammatory; anti-anemic; antidiabetic; 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 361 KAKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS ö LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470 Indels Humanised HFE7A designed heavy chain HHH type protein. 2; Mismatches AAW90936 standard; Protein; 470 AA (first entry) Conservative 08-AUG-2000 Matches 466; Synthetic. AAW90936; RESULT 10 421 301 AAW90936 qq ò g Pp g g g δy ò g ò ð ò g ŏ

98JP-0276882. 99EP-0307711 98JP-0276881 CO LTD. (SANY ) SANKYO 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; EP990663-A2. 05-APR-2000.

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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

cappotosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-infilammatory,

anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antirheumatic, nephrotropic, antilifertility, neuroprotective,

antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

antiarteriosclerotic, cardiant and hepatropic activity, (I) induce

continued to cell surface Fas or inhibit it by competitive

inhibition of ligand binding. (I) are used to treat and/or prevent

continued that the Fas/Fas ligand system, especially systemic

diseases associated with the Fas/Fas ligand system, especially systemic

cupus errythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

classase, autoimmune hemolytic anemia, sterility, myasthenia gravis,

multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

CB, Cor D) or alcoholic,, and transplant rejection.

(B, Cor D) or alcoholic, and transplant rejection.

(B, Cor D) or alcoholic, and transplant rejection or himbormal

cells. They bind to both human and murine Fas, so can be evaluated in

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

the native disease model the produce of the active site of Fas, i.e. they mimic

the native disease.

characterial of the human anti-murine antibody response. This sequence represents

which is decribed.
                                                                                                                                                                         humanized anti-Fas antibody, useful for treating or preventing e.g. ammatory or autoimmune disease, induces apoptosis selectively in
                              Ë
                              Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which is described in the method of the invention.
                           Tamaki I,
                                                                                                                                                                                                                                 cells with abnormal Fas-Fas ligand systems
                              Α,
                                                                                                                                                                                                                                                                                               Claim 2; Page 188-189; 263pp; English.
                              Nakahara
                              H,
                                                                                   2000-258930/23
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470 AA; Sequence

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                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                   GQGLEWMGEIDPSDSYINYNQKFKGKATLIVDISTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                           KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                      Gaps
                                           9
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                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                   WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                      YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                      ö
   Length 470;
                      Indels
  DB 21;
 Score 2498; DB 21;
Pred. No. 2.5e-143;
                     3; Mismatches
99.2%;
          al Similarity 98.9
465; Conservative
  Query Match
            Local
            Best Loca
Matches
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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-2ABM5168 and encoded by ABA02682-ABA02128. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                         Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvs 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                         LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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es 10;
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Pred. No. 3.86
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                                                                                                                          AAM52156 standard; Protein; 731
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02-OCT-2000; 2000US-237159P
                                                                                                                                                                                    (first entry)
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les 438; Conserv
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                                                                                                                                                                                                                                                                                                                                              Humanised monoclonal antibody; polymorphic epithelial mucin; PEMI;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
300
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                                              KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                               YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                            KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                       421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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02-OCT-2000; 2000US-237159P
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                                                                                                                                                                                                                                                                                                   (first entry)
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Gaps

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Indels

Length 741;

DB 22; 10;

93.3%; Score 2349.5; DB 2793.2%; Pred. No. 3.8e-134; ive 19; Mismatches 10;

438; Conservative

Similarity

Query Match Best Local Matches 43

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nonoclonal antibody; polymorphic epithelial mucin; PEM1; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                                 180
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                                     GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                   YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised monoclonal antibody;
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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02582-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                                                                                    DB 22; Length 729;
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                                                                                                 93.1%; Score 2344.5; DB 2:93.2%; Pred. No. 7.5e-134; ive 19; Mismatches 10;
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                                                                                                            Local Similarity 93.2 nes 437; Conservative
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02-OCT-2000;
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cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                               Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity follymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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                                                                                                                                                                                                                                                                                 Score 2344.5; DB 2:
Pred. No. 7.6e-134;
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                                                                                                               Claim 20; Figure 12; 176pp; English
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93.2%;
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                       WPI; 2001-662969/76.
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93.2%; Pred. No. 1.7e-133;
tive 19; Mismatches 10;
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Matches 436; Conservative
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Search completed: August 14, 2002, 15:15:40 Job time: 838 sec

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LENGTH: 449 amino acids TYPE: amino acid
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1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
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US-09-049-672A-8
US-09-027-449-71
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US-09-485-737B-67
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US-08-887-352B-14
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STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                      PCT US93 07832 23
US-07-914-373-23
US-09-247-352-3
US-09-247-352-3
US-08-157-101A-7
US-08-157-101A-7
US-08-704-672A-4
US-08-341-560B-17
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US-08-461-968A-5
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
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Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antib
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
STREET: One Market F
CITY: San Francisco
STATE: California
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5

Gaps

5

Length 449; Indels

88.8%; Score 2235; DB 1; 93.3%; Pred. No. 6.6e-159; live 13; Mismatches 15; Ξ

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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                          179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
                                                                                                                                                                                                                                                                                                                                                    NQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
                                                                                                                 140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                           SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259
20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08378939
Patent No. 5876910
GENERAL INFORMATION.
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                              419 WQQGNVFSCSVMHEALHNYTQKSLSLSPGK 449
                                                                                                                                                                                                                                                                                                                                                                                                               440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WHEER: US 07/952640
FILING DATE: 01-DEC-1992
ATTONEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1808-118 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 783-6040 TELEFAX: (202) 783-6031 INFORMATION FOR SEC ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 476 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20004
COMPUTER READABLE FORM:
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TOPOLOGY:
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US-08-378-939-10
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61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNR- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 -----DYSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 414
                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Rarl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Panghn, Mariah R.
APPLIC
                                                                                                                                                            Length 476;
                                                                                                                                                FastSEQ for Windows Version 2.0
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/049,672A FILING DATE: HEREWITH CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                     Best_Local Similarity 88.7
Matches 422; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                us-08-378-939-10
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US-09-049-672A-8
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                                                                                                                                                                    Query Match
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
 South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 408; Conservative
                                                       COMPUTER READABLE FORM:
                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                          94080
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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US-09-026-985-71
                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 MGEIDPSDSYTNYNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 426
                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                              87.6%; Score 2205.5; DB 4
89.4%; Pred. No. 1.1e-156;
iive 18; Mismatches 28;
                                                      39,132
R: PF-0497
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Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
                                     NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/COCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Genentech, Inc.
1 DNA:Way
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CEITODE, Michael C
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.4 Matches 415; Conservative
                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
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; CLONE: 2747531
US-09-049-672A-8
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80 NOKFKGKATLIVDISISTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGTLVIV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMTKNQVSLITCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
COMPUTER: ACADALE FORM:
COMPUTER: ACADALE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
FILING DATE: 20-Feb-1998
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET UNMBER: 91085R3-2
TELECOMMUNICATION INFORMATION:
TELEDRANCE/DOCKET UNMBER: p1085R3-2
TELEDRANCE/DOCKET UNMBER: p1085R3-2
TELEDRANCE/DOCKET UNMBER: p1085R3-2
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90.3%; Pred. No. 1.5e
tive 26; Mismatches
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421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
                                                                                           Sequence 67, Application US/09485737B Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 90, Application US/09485737B
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.0
SEQ ID NO 67
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: SYNTHETIC US-09-485-737B-67
                                                                                                                                          APPLICANT: Buyse, Marie-Ange APPLICANT: Sablon, Erwin
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 104
                                                                                                                          GENERAL INFORMATION:
                                                                             US-09-485-737B-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                            APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.5%; Score 2203.5; DB 4; Best Local Similarity 90.3%; Pred. No. 1.5e-156; Matches 408; Conservative 26; Mismatches 17;
                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/026,985 FILING DATE: 20-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 10085R3-1
TELECHONE: 650/225-5530
TELEPHONE: 650/255-5530
TELEFAX: 650/255-9881
INFORMATION FOR SEO ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
Sequence 71, Application US/09026985 Patent No. 6133426 GENERAL INFORMATION:
                                                                                                                                                        Genentech, Inc.
                                                                                                                                                                                     South San Francisco
                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                      1 DNA Way
                                                                                                                                                                                                     California
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STREET: 1
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APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT FILING DATE: 1000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1999-06-18
PRIOR FILING DATE: 1997-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 86.4%; Score 2174; DB 4; Best Local Similarity 88.0%; Pred. No. 2.5e-154; Matches 409; Conservative 21; Mismatches 31;
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COMPUTER: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POF WARD DEPARTMENT OF THE SUPPLIANCE OF THE STATEM OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE STATES OF SOFTWARE SO
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
     Genentech, Inc.
DNA Way
                                                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.8%;
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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Best Local Similarity
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ADDRESSEE:
STREET: 1
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                                                                                APPLICANT: BUYSE, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: POT/EP 98/05165
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
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Sequence 22, Application US/0793
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                                                                                                                                                                                                                                       TVSSASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
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                                        Indels
; Score 2158.5; DB 2; Pred. No. 3.4e-153; 18; Mismatches 28;
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377 SREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
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                                                                                            EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 15.25 inch, 360 Kb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRE
                                                                                                                                                                                                                                                                                                                                             437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-7UN-1992
FILING DATE: 15-7UN-1992
PRIOR APPLICATION UNBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
                                                         Sequence 22, Application US/08437642B
Patent NO. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICE APPLICATION DATA.
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40,378
ER: P0709P2C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,378
REFRENCE/POCKET NUMBER: P070
TELECOMMULAATION INFORMATION:
TELEPHONE: 650/225-1994
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 454 amino acids
Amino Acid
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US-08-437-642B-22
                         US-08-437-642B-22
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LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 256
                                                                                                                                                                 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                             EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
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                                                                                                                                                                                                                                                                                                    TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: EDELMAN, LENA
APPLICANT: MAGCARITTE, CHRISTEL
APPLICANT: MACZOREK, MICHEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS ITILE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: US/08/793,450 FILING DATE: 03-MAR-1997 PRIOR PATE: 536
                                                                                                                                                                                                                                                                                                                                              437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                             421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
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APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08793450 Patent No. 6312690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 472 amino acids
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STATE:
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Sequence 14, Application US/08887352B

Patent No. 5994511

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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                                                                                                                                                                                                                                                      61 GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                              236 KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
                                            Gaps
                                                                                                           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
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    Length 472;
                                         Indels
85.3%; Score 2147; DB 4;
85.1%; Pred. No. 2.6e-152;
live 26; Mismatches 37;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul 1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: South San Francisco
STATE: California
COUNTRY: USA
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  Query Match 85.35
Best Local Similarity 85.15
Matches 404; Conservative
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INFORMATION FOR SEQ ID NO:
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TELEFAX: 65
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US-08-887-352B-14
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CLASSIFICATION:
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                                                                   120 SSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179
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                                                                                                                                                                                                                                                                                                                  139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                    199 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
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                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
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                                                                                                                  Length 451;
                                                                                                                84.5%; Score 2127; DB 2;
87.8%; Pred. No. 7.4e-151;
tive 23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: US/08/887,352B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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03-Jul-1997
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ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                   Conservative
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Matches 397; Conser
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ZIP: 94080
                                                                 US-08-887-352B-14
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120 SSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179
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                                                                                                                                                                                                                                               Length 451;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                           Query Match 84.5%; Score 2127; DB 2; Best Local Similarity 87.8%; Pred. No. 7.4e-151; Matches 397; Conservative 23; Mismatches 30;
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: Amino Acid

US-08-887-352B-16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATA
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SOFTWARE: WinPatin
CURRENT APPLICATION DAY
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-466-151-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Gaps

5

Indels

30;

Length 451;

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YNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                           20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1-451
COTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14
                                                                                                                                                                                                                                    84.5%; Score 2127; DB 4;
87.8%; Pred. No. 7.4e-151;
live 23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/109,207C
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,20:
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 14, 2002, 15:17:08 Job time: 691 sec
                                                                                                                                                                                                                                                  Best_Local Similarity 87.8
Matches 397; Conservative
                                                                                                             TYPE: PRT ORGANISM: Artificial
                                                                                                                                                    NAME/KEY: Artificial
                                                                                                                                                                                                                                       Query Match
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 YNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
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87.8%; Pred. No. 7.4e-151;
tive 23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P0718P2C1D1
                                                                                           FILLING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09109207C Patent No. 6172213
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-ig
                                           FILING DATE: 15-MAK-LOUGH APPLICATION DATA:
APPLICATION NUMBER: 08/185899
                          06-Jun-1995
NUMBER: 08/405617
15-MAR-1995
                                                                                                                                                                                                       NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9811
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                397; Conservative
             APPLICATION NUMBER:
FILING DATE: 06-Jur
                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 397; Conserva
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US-09-109-207C-14
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:19:01; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-499-662-147 2517 1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\* Database

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description		gamma	Ig gamma-3 chain C					Ig gamma-2b chain				-		~	Ig gamma 2a chain			O				Ig gamma-2 chain C		gamma-3					Ig gamma-1 chain C	
SUMMARIES	ID		CHHO	A23511	A60764	S37483	G2HU	G4 HU	G2MS11	S40295	S01321	822080	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	GIMS	PS0018	GIMSM	G3MSM
	DB	!	٦	7	7	7	Н	1	1	~	7	7	~	7	7	ď	7	4	~	7	-	7		7	-	7		Н	~	<del></del> 4	Н
	Length		330	377	377	469	326	327	474	446	475	470	472	374	444	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
,	% Query Match		8.69	65.1	65.1	64.0	64.0	63.5	61.4	61.3	59.7	58.7	58.4	57.0	56.8	50.3	50.1	49.8	49.5	49.1	48.9	48.9	48.1	46.3	46.0	45.9	45.7	45.5	45.5	45.3	45.3
	Score	1 1 1 1 1 1	1758	1639.5	1637.5	1610.5	1610	1599.5	1546	1544	1501.5	1477	1470	1435	1429.5	1267	1261	1253	1245	1235	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	1144.5	1140	1139
	Result No.		п	7	n	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

A)Contents: Eu
A)Accession: A90564
A; Molecule type: protein
A; Residues: 136-154, 'O', 156-165, 'O', 167-176, 'O', 178-194,'N', 196-197, 'D', 199-238,'E', 2
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
B; Ponstingl, H.; Hilschmann, N.
H)Appe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgGI-Immunglobulins (Myelomprotein Ni

Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
G2MSA	S00847	G2MSAB	G2MSAM	PS0019	S06611	GZMSBM	147162	S38864	S14683	S04845	S69131	S38950	A4944	569340	B46529
7	7	н	Н	7	7	Н	7	7	7	7	7	7	7	7	7
330	329	335	399	322	327	405	277	548	627	549	241	246	220	249	572
44.9	44.8	44.8	44.7	44.3	43.4	42.9	42.5	39.7	37.6	36.8	34.6	33.8	31.8	30.4	30.3
1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	666	946	925.5	870.5	851	801	765.5	762.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1 GHHU Ig gamma-1 chain C region - human
	C;Species: Homo saplens (man) C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
	R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982
_	A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238
	A; Accession: A93433
	A;Molecule type: DNA A:Residues: 1-330 <fll></fll>
	A;Cross-references: EMBL:217370
	A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A:Note: Lys-330 is removed after translation
	R; Harris, L.J.
	submitted to the EMBL Data Library, October 1992
	A; Reference number: \$33904
	A; Accession: S36861
	A; Molecule type: DNA
	A;ResIdudes; 2-330 (AHAK> A.Cosserpeferences : EMB: 217370
	R. Tarbon T.
	Cell 29, 671-679, 1982
	A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of
_	A; Reference number: S33887; MUID:83001943
-	A; Accession: S33887
	A; Molecule type: DNA
_	A; Residues: 88-113; 235-330 < TAK>
	A; Cross-references: EMBL: 21/3/0
	A/CURINIGHAMIA D.A.; NULTBIAGSEL, U.; GAIL, W.E.; GOLLIED, F.U.; MAXUAI, M.U.; EUGLMA RICCHEMISTTV 9, 3161-3170, 1970
	A; Title: The covalent structure of a human qammaG-immunoqlobulin. VII. Amino acid seq
	A; Reference number: A90563; MUID:71064024
-	A;Contents: myeloma protein Eu
-	A; Accession: B90563
	A; Molecule type: protein
	A; Residues: 1-96, 'R', 98-135 <cun></cun>
	A; Note: this sequence has the Glm(3) marker, 97-Arg
	K;KULIShauser, U.; Cuminingnam, B.A.; Bennert, C.; Konigsberg, W.H.; Edelman, G.M. Bishemistru G. 3171-2101 1070
	DIOCHEMISELY 9, 31.1.3.11.2.301, 1970. DIOCHEMISELY 9, 31.1.3.11.2.301, 1970. DIOCHEMISELY 9, 31.1.3.11.2.11.2.1.2.1.2.1.2.1.2.1.2.1.2.1.2.1.2.1.2.1.2.1.2.1.2
	A:A:LIE: 11e COVAIGHL SILECTER OI A HUMAN GANNING LINNING LOUGHTIN. VIII. ANIIN ACIA SE A:Asferance number: 100564. MITD:71064035
_	A VETELEUCE HUMBEL. DOCOS, MOLD., LOCACEO

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:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSTYRVVSVLIVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 377;
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-377 < HUC>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Tetle: A human immunoglobulin IGHG3 allele
A;Reference number: A60764; MUID:90007613
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Best Local Similarity 82.8
Matches 312; Conservative
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                                                                       A. Moclesula in Bylone
B. Schmidt, W. E.; Juny, H. D.; Palm, W.; Hilschmann, N.
B. Schmidt, W. E.; Juny, H. D.; Palm, W.; Hilschmann, N.
B. Schmidt, W. E.; Juny, H. D.; Palm, W.; Hilschmann, N.
B. Schmidt, W. E.; Juny, B. D. Bylone
A. Reference number: Api123, WID: 8124911isierbaren monoklonalen Immunglobulins IgG1 KOI
A. Reference number: Api123, WID: 8124911isierbaren monoklonalen Immunglobulins IgG1 KOI
A. Reference number: Api123, WID: 8124911isierbaren monoklonalen Immunglobulins IgG1 KOI
A. Reference number: Api23, WID: 8124911isierbaren monoklonalen Immunglobulins IgG1 KOI
A. Reference number: Api346, 1970
A. Title: The covalent Extructure of a human gammad-immunoglobulin. X. Intrachain disulfide
A. Reference number: Api365, WID: 7107026
A. Contents: annotation: disulfide bonds
B. Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
B. Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
B. Hoppe-seyler's Z. Physiol. Chem 377 1515-1540, 1976
A. Contents: annotation: disulfide bonds
A. Reference number: Algority and the disulfide bridges.
A. Contents: annotation: disulfide bonds
A. Reference number: Algority and the disulfide bonds
A. Reference number: Algority and the disulfide bonds
A. Reference number: Algority and the disulfide bonds
A. Moclesulists
A. Complex: An immunoglobulin hemology (AM2)
A. Complex: An immunoglobulin hemology (AM2)
F. 24-310/comain: immunoglobulin homology (AM2)
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F. 109. 112-Dis
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Pred. No. 3.3e-93;
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     MUID:77070269
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99.1%;
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A, Reference number: A91668;
A, Contents: myeloma protein
A, Accession: B91668
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 537483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: 537483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-69 < DUC>
A;Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology < IMM>
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llarity 64.4%; Pred. No. 1.2e-84;
Conservative 60; Mismatches 103; 1
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                                                    Score 1637.5; DB Pred. No. 2.8e-86; 7; Mismatches 11
                                                                                                                                                          201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV---
                <IWW>
C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology
                                                    Query Match 65.1%;
Best Local Similarity 82.8%;
Matches 312; Conservative
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A; Modecule type: protein
A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 11,
A; Rotace: this sequence has since been revised
A; Note: this sequence has since been revised
B; Hofmann, T.; Parr, D.M.
MOI. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A; Reference number: A93132; MUID:80114419
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A; Residues: 1-326 <ELL>
A; Cross references: GB: V00554; GB: J00230; NID: g32759; PIDN: CAB58438.1; PID: g6066056
A; Note: Lys 326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human 1gG2 heavy chain: genetic, evolutionary, a A; Fitle: The primary structure of a human 1gG2 heavy chain: genetic, evolutionary, a A; Contents: myeloma protein Til
A; Accession: A92809
A; Accession: A9280
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C; Species: Homo sapiens (man)
C; Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C; Accession: A93906; A92809; A90752; A93132; A02148
R; Ellisson, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy of A; Reference number: A93906; MUID: 82197621
                                                                                                                                                                                                                                      297
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G3. A;Feference number: A90253; MUID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
KSCDKTHTCPP - - CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                               ISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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A; Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A; Reference number: A94591
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Gaps

3;

320

117

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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C; Accession: $25057; A26235; A26232; A26233; A53598
R; Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A; Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi A; Reference number: $25057
A; Accession: $25057
A; Accession: $25057
A; Accession: $25057
A; Residues: 1-474 AFIS>
A; Res
                                 A map position: 14932,33-14932.33

A introns: 99/1; 111/1; 221/1

A introns: 99/1; 111/1; 221/1

A introns: 99/1; 111/1; 221/1

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 
C; Superfamily: immunoglobulin c region; immunoglobulin homology 
C; Keyvords: duplication; 91/20protein; heterotetramer; immunoglobulin 
F; 20-85/Domain: immunoglobulin homology <IM1>
F; 99-110/Region: hinge 
F; 134-203/Domain: immunoglobulin homology <IM2>
F; 140-307/Domain: immunoglobulin homology <IM3>
F; 141-201, 247-305/Disulfide bonds: interchain (to heavy chain) #status experimental F; 177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 PSVFLFPPKRVDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177
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A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1599.5; DB 1;
Pred. No. 3.4e-84;
9; Mismatches 15;
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OMIM: 147130
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Best Local Similarity 91.8%;
Matches 303; Conservative
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A; Map position:
A; Map posit
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C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
C;Accession: A90933; A90249; A02150
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440
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A.Molecule type: DNA
A.Rosidues: 1.327 CELLA
A.Note: the sequence was determined from the germline gene
R.Note: the sequence was determined from the germline gene
R.Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Blochem. J. 117, 33-47, 1970
A.F. Sinchem. J. 117, 33-47, 1970
A.R. Seference number: A90249; MUID:70207560
A.Rolecule type: protein
A.Residues: 1-30;81-326 <PIN>
C.G. Genetics:
A.Genetics:
A.Genetics:
A.Genetics:
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                                               Ö
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                                          of immunoglobulin
MUID:69064124
disulfide bonds
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                                          A;Title: Structural studies
A;Reference number: A93157;
A;Contents: annotation; Sa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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C; Accession: S40295
R; Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C., Submitted to the EMBL Data Library, January 1993
A; Reference number: S40295
A; Accession: S40295
A; Molecule type: protein
A; Residues: 1-446 < KLE>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin C region; immunoglobulin pyroglutamic acid
C; Superfamily: immunoglobulin c region; immunoglobulin; pyroglutamic acid
E; 1-46/Product: Ig gamma-2a chain #status experimental <MAT>
F; 1-117/Domain: U-5-J region <VDJ>
F; 118-46/Domain: C region <CHR>
F; 118-44/Domain: C1 region <CHI>
F; 215-230/Region: hinge
F; 231-340/Domain: C3 region <CH2>
F; 341-46/Domain: C3 region <CH2>
F; 350-427/Domain: C3 region <CH2>
F; 360-427/Domain: Immunoglobulin homology <IMM>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F; 220-56, 144-199, 261-321, 367-425/Disulfide bonds: #status predicted
F; 224, 227, 229/Pisulfide bonds: interchain (to light chain) #status predicted
F; 224, 227, 229/Pisulfide bonds: interchain #status experimental
F; 297/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
                                                                                                         PIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 NOKFKGKATLIVDISISIAYMELSSLRSEDIAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                   414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                   D-LYTLSSSVIVYSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNL
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64.4%; Pred. No. 7e-81;
Live 59; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-2a chain (mAb735) - mouse
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Best Local Similarity
Matches 291; Conserv
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A,Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heal A;Ritle: Structure of the constant and 3' untranslated regions of the murine gamma2b heal A;Conneits: MC 13
A;Conneits: MC 14
A; Response 14 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 44 As probaby removed posttranslationally
B; MC 26: LD 4, 174-189, FP', 193-376, 'T', 378-474 <TU2>
A; MC 26: LD 10A
A; MC 26: LD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.4
Best Local Similarity 61.2
Matches 292; Conservative
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C;Accession: $22080; $06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: $22080
A;Reference number: $22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1470 <SAN>
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
A;Cross-reference number: $06610; MUID:90097956
A;Accession: $06610
A;Molecule type: DNA
A;Reference number: $06610; MUID:90097956
A;Accession: $06610
A;Molecule type: DNA
A;Residues: 142-470 <SXN>
A;Res
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Sacession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNR--D 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 -TC-KPSPCDCCPPPELPGGPSVFIFPPREMENTITISGTPEVTCVVVDVGHDDPEVKFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ALEWVGGI-TSGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane [F:161-225/Domain: immunoglobulin homology <IMM>
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
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58.7%; Score 1477; DB 2;
Best Local Similarity 60.4%; Pred. No. 4.8e-77;
Matches 285; Conservative 62; Mismatches 115;
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N;Alternate names: 1g gamma-1 chain C region (clone 8.10)
C;Species: Bos primiqenius turuus (cattle)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 V-GLLPFGYNGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
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60.6%; Pred. No. 2e-78;
ive 66; Mismatches 113; Indels
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                                                                                                                                        438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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C. Species: Homo sapiens (man)
C. Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C. Accession: S69339; S72664
R. Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A. Fitle: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A. Reference number: S69339
A. Reference number: S69339
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-374 < KHA>
A. Cross-references: EMBL: X81695
R. Khamilchi, A.A.
Submitted to the EMBL Data Library, September 1994
A. Reference number: S72664
A. Reference number: S72664
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-140, 'C', 142-374 < KH2>
A. Status: preliminary
A. Residues: 1-140, 'C', 142-374 < KH2>
A. Status: preliminary
A. Status: pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
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                                                                                                                               homology
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                A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-472 - CPAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin
C;Keywords: immunoglobulin pomology <IMM>
                                                                                                                                                                                                                                                           tch 58.4%; Score 1470; DB 2; I al Similarity 59.6%; Pred. No. 1.2e-76; 283; Conservative 66; Mismatches 114;
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277-346/Domain: immunoglobulin homology <IMM>
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Best Local S
Matches 283
A; Accession:
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
G;Species: Mus musculus (house mouse)
G;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
G;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porf-A;Recession: PC4436
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag C;Comment: This catalytic antibody in mmunoglobulin c region; immunoglobulin homology cimp. F;251-320/Domain: immunoglobulin homology <IMD. F;22/Disulfide bonds: interchain (to 98) #status predicted F;99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                     4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 AKGOPREPQVYTLPPSREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 421
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                                                                                 Gaps
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                                                                                                                                                                   5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMQWVRQAPGQ
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Length 374;
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Score 1435; DB 2;
Pred. No. 9.2e-75;
7; Mismatches 58;
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58.0%; Pred. No. ...
79; Mismatches
                                                                             27;
    57.0%;
60.1%;
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        Query Match
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                                               Best Loca
Matches
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A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domaln: immunoglobulin homology <IMM>
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Best Local Similarity 69.68,
Matches 231; Conservative
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C; Species: Sus scrofa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147159
R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Titler: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147158; MUID:95012845
A; Accession: 147159
A; Accession: 147159
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VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CP 253
                                                                                                    APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
                                                                                                                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 373
                                                                                                                                                                                                                                      LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 433
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                   434 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Mismatches
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les 232; Conserv
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Best Local S:
Matches 232
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of cDNA sequences Ig gamma 2b chain constant reyrow fer (domestic pig) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-C;Accession: I47160
R;KacsKovics, I; Sun, J.; Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the A;Reference number: I47158; MUID:95015845
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>

Gaps 9; Length 328; Indels 54; ; Score 1261; DB 2; ; Pred. No. 6.4e-65; 41; Mismatches 54;

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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380

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-I- MISCELLANBOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
-I- MISCELLANBOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 155,166,177,195,198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                                                                                                                                              "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-% resolution."; Biochemistry 20:2361-2370(1981).
                                                  Dreker L., Schwarz J., Reichel W., Hilschmann N.;

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Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SWART; SM00407; IGclike; 1.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 30-structure.
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REMOVED POST-TRANSLATIONALLY.

K -> R (IN GIM(3) MARKER).

/FTIG=VAR_003886.

D -> E (IN GIM(NON-1) MARKER).

L -> M (IN GIM(NON-1) MARKER).

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MEDLINE-81208100; Pubmed=7236608;
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PIR; A02146; GHU.
PDB; IFC1; I5-JUL-92.
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MEDLINE=77070267; PubMed=1002129;
          Biochemistry 9:3188-3196(1970).
Intrachain disulfide bonds.";
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21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1G gamma-2 chain C region.
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MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
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Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human igG2 myeloma protein.";
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                                              Ellison J.W., Hood L.E.; "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes."; Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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MEDLINE-83001943; PubMed-6811139;
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                                                                                                                                                                                                                                                                                                                                                 Wang A.-C., Tung E., Fudenberg H.H.;
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evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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Hofmann T., Parr D.M.;
A note of the amino acid sequence of residues 381-391 of limmunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                            SEQUENCE OF 99-177 AND 310-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
MEDLINE=81007873; PubMed=6774012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
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                        SEQUENCE OF 2-326 FROM N.A. MEDLINE-82197621; Pubmed-6804948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=72033500; PubMed=4940472;
                                                                                                                                                                         evolution of a gene family.";
Cell 29:671-679(1982).
                                                                                                            SEQUENCE OF 88-115 FROM N.A.
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SEQUENCE OF 238-275 (ZIE)
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                                                                                                                                                                                                                                                                                                  EMBO J. 1:403-407(1982).
 NCBI_TaxID=9606;
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C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
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Pred. No. 8.9e-104;
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83
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326
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MIM; 147110; -.
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GC_RABIT
P01870:
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MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                   Ellison J.W., Buxbaum J.N., Hood L.E.; "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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INTERCHAIN (WITH A HEAVY CHAIN)
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1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Immunoglobulin C region.
 16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                    EMBL; K01316; AAB59394.1; ALT_INIT.
                                                                                SEQUENCE FROM N.A.
MEDLINE-83157104; PubMed-6299662;
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                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003607; Ig_like.
Pfam; Pr00047; Ig; 3.
SMART; SM00407; IG_like; 1.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 2.
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91.8%;
         gamma-4 chain C region
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                              Homo sapiens (Human)
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HSSP; P01842; 7FAB.
MIM; 147130; -.
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
HISCELANDENGE: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
MARKERS AND REF.5 THE E15 MARKER.
                                                                                                            MIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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"Sequence studies of the Fd section of the heavy chain of rabbit
imminariand "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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MEDLINE=76135469; Pubmed=1243651;
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
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Biochemistry 10:26-31(1971).
-!- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 IMPRED GUINEA PIGS.
PIR; A02151; G2GP.
                                                                                                                                                                                                                                                                                                                                    MEDLINE-71058474; PubMed-4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
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Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 134-226.
MEDILINE-7036072; Pubmed-4429665;
Tracey D.E., Cebra J.J.;
"Primary Structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                            SEQUENCE OF 227-311.
MEDLINE-7036073. Pubmed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig 19G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTH--TCPPCPAPEL
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; Pred. No. 2.6e-76;
30; Mismatches 62; Indels 9;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
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                                                                    SEQUENCE OF 69-133 AND 312-329.

MEDLINE-71058466; PubMed=5538616;

Turner K.J., Cebra J.J.;

"Structure of heavy chain from strain 13 guinea i immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";

Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                      Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                    Biochemistry 13:4804-4811(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P01772; ZFB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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329 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                        Query Match 48.9%; Score 1231.5; DB 1; Length 323; Best Local Similarity 70.0%; Pred. No. 9.1e-78; Matches 229; Conservative 34; Mismatches 57; Indels 7;
                                                                  M (IN D11 MARKER).

A (IN B15 MARKER).

E (IN REF. 2).

VPV (IN REF. 2).

E (IN REF. 5).

C (IN REF. 5).

D (IN REF. 5).

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C (IN REF. 5).

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C (IN REF. 5).
                                                                                                                                                                                                                                                       69E8AA118D579A8B CRC64;
                                              Immunoglobulin domain; Immunoglobulin C region.
NON.TER 1
1 104 T -> M (IN D11 MAR!
VARIANT 185 185 T -> A (IN D15 MAR!
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
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Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 NVFSCSVMHEALHNHYTQKSLSLSPGK 470
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MEDLINE=71058471; PubMed=5538606;
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                         100407; IGC1; 2.
PS00290; IG_MHC; 1.
 InterPro; IPR003597; Ig_c1
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173
187
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256
260
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              Pfam; PF00047; ig;
SMART; SM00407; IG
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P01862;
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                           235
                                                       378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 435
                                                                      318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NORMALLY PRESENT IN THE HINGE REGION.
MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-3 HEAVY CHAINS.
MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                              Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Prihany structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                MEDLINE-82247835; PubMed-6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 12-97 OF PROTEIN WIS.
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Franglone B., Franklin E.C.;
Primary structure of the 'hinge' region of human igG3. Probable quadrupilcation of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-301 (Rel. 40, Last annotation update)
169 gamma-3 chain C region (Heavy chain disease protein) (HDC)
1GHG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Franglone B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein 20C. Structure of the Fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC)
                                                                                                               DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
                                                                                                                               296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
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MEDLINE-81021548; PubMed-6774747;
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                                                                                                                                                                                                                STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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/FTId=VAR_003891.
F -> Y (IN OMM).
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S -> N (IN OMM).
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T -> A (IN OMM).
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                                                                                                                                                                                         Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
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SSP; P01857; 1FC1.
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MIM; 147120;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-1 chain C region.
Rattus norvegicus (Rat).
Elwaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
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                                                                                                                                                                                         "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 SEVSSVFIFPPPRFKDVLTITLTFKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 ISKTKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESSGOPENNYNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
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                         INTERCHAIN (WITH A HEAVY CHAIN).
                419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                  C region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                          45.9%; Score 1155; DB 1; Length 326; 63.4%; Pred. No. 1.7e-72; Live 52; Mismatches 60; Indels 1
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                                                                         326
                                                                                                                                                                                                                                                                  Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                         HINGE.
CH2.
                                                                         PRT;
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed-3149946;
Brueggemann M.;
                                                                                                                                                                                                                                                                                                          CH3.
                                                                                                                                                                                             Gene 74:473-482(1988)
PIR: PSO017: PSO017
HSSP; PO1842: 7FAB.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
SMART: SM00407; IgG: 3
PROSITE: PS00299: IG_MHC; 1.
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326 AA;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. WEDLINE 8502161; PubMed=6092053; WEDLINE 8502161; PubMed=6092053; Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01857; IECI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003509; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
IMMINOSITE; PS00299; IGMHC: 1.
Imminoglobulin domain; Immunoglobulin C region; Glycoprotein; Iransmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 329;
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65.0%; Pred. No. 3.7e-72;
ive 44; Mismatches 68;
                                                                                                                                                                                                                                  update)
                                                                                                                                     329 AA
                                                                                                                                                                                                       Last sequence update)
294 EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 326
                                                                                                                                                                                                                                                     Ig gamma-3 chain C region, secreted form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                    Last annotation
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HINGE.
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Matches 215; Conserv
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                               01-AUG-1991 (
01-AUG-1991 (
16-OCT-2001 (
                                                                                                                                   GC3_MOUSE
P22436;
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SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDILE-80012837, PubMed-113776;
ROGERS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-8020559; Pubbled-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma i heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
10 gamma-1 chain C region.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                            'Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFIDE BONDS (MOPC 21).
MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                     Kawakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primary structure of
                                                                                                                                                                                                                                                                                                                  MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T.,
Takahashi N., Mano Y.;
                                                                                                                                                     324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adetugbo K.; "Evolution of immunoglobulin subclasses.
                                                                       299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                       440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 6:3305-3321(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
[5]
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EMBL; V00793; CAA24174.1; -.
EMBL; V00795; CAA24175.1; -.
EMBL; V00795; CAA24176.1; -.
PIR; A02159; GIMS.
HSSP; P01842; 7FAB.
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                                                                                                                                                     STANDARD;
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Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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P01868;
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GC1_MOUSE
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115 --SSVFIFPPREMENDVLITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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CHAIN).
CHAIN).
GlycoSuiteDB; P01868; -.
MGD: MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_Cl.
Pfam; PF00047; ig; 3.
SWART; SMO407; IGC.1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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INTERCHAIN (WITH A HEAVY
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region.
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MEDLINE-89232738; Pubmed-3149946;
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Matches 207; Conservative
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                                                                                                                               Alternative splicing.
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276
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324 AA;
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P20761;
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Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74.473-482(1988). PPR: PSO018; PSO018; PSO018. HSSP; PO1842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
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30-MAY-2000 (Rel. 19, Last sequence update)
Ig gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Musimae; Mus
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MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                               CHAIN).
CHAIN).
CHAIN).
                                                                                                                                                                                                                                                                                                                                      Length 333;
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                                                                                                                                                                                                                                                                                                                                     45.5%; Score 1144.5; DB 1; Length 63.7%; Pred. No. 9e-72; ive 45; Mismatches 68; Indels
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                                                                                                                                               PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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01-AUG-1991 (Rel. 19, Last seq
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333 AA;
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                                                                                                                                                                                                                                                                                                     Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoapilobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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                                                           Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
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                                                                                                                                                  SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; Pubmed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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4CC88343B7A1CE27 CRC64;
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                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
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62.2%; Pred. No. 2.3e-71;
tive 55; Mismatches 60;
Cell 18:559-568(1979).
[2]
SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed=6804950;
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MEDLINE-82222190; PubMed=6283537;
                                                                                                                                                                                                                               immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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393 AA;
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

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                                                                                                                  201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
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                              259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
   ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Musinse
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MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
HSSP; P01687; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_Like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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P03987;
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SECUENCE FROM N.A.
MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP--PCPAPELLG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                            Length 398;
                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
R; CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Match 45.3%; Score 1139; DB 1; Local Similarity 64.7%; Pred. No. 2.7e-71; es 213; Conservative 44; Mismatches 68;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-MAY-2000 (Rel. 39, Last annotation update)
1g gamma-2A chain C region, A allele.
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                      Alternative splicing
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                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
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MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
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MEDLINE-7417517; PubMed-4831970;

MEDLINE-7417517; PubMed-4831970;

BOUTGOIS A., Fougereau M., Rocca-Serra J.;

"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";

BLUT. J. Blochem. 43:423-435(1974).
                                    suggests that exons can be exchanged between genes in a multigenic
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                                                                                                                                                                                                              "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Biochem. 30:452-462(1972).
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INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
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B84361C5445A6864 CRC64;
                                                         Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                        MEDLINE-73056887; PubMed-4565406;
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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Best Local Similarity 63.99
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330 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2C chain C region.
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                                                                                                                                       299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
                                                                                                          RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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HINGE.
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MEDLINE=88166903; Pubmed=3127222;
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HSSP; P01857; 1FC1.
InterPro; 1FR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003509; Ig_like.
Pfam; PF00047; ig; 3.
SMART; $M00410; IG_like; 1.
SMART; $M00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                    LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
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DODILD M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine gamma 2a heavy chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-40355(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D Schreier differences between the nucleic acid sequences of IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-399 (Arel. 38, Last annotation update)
Mus musculus (Mouse)
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HSSP; P01857; IFC1.
InterPro; IPR0035006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003500; Ig_Like.
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SMART; SM00410; IG_like; 1.
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P01864;
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GCAB_MOUSE
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Score 1126.5; DB 1; Length 335; Pred. No. 1.6e-70;

44.88;

Best Local Similarity

Query Match

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141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK-----SCDKTHTCPPCPA 254
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7; Gaps
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70;
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Mismatches
52;
Conservative
Matches 207;
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1 MGWSCIILFLVATATGVHSQ.......MHEALHNHYTQKSLSLSPGK 470
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL_19:*

1: sp_bacteria:*

3: sp_bacteria:*

5: sp_fungi:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_invertebrate:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

2: sp_vertebrate:*

3: sp_vertebrate:*

3: sp_vertebrate:*

3: sp_vertebrate:*

5: sp_roins:*

5: sp_roins:*

7: sp_roins:*

8: sp_roins:*
                                                                                                                                                                                                                                                                                                                   BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	O9d814 mus musculu	Q991c4 mus musculu	Q99125 mus musculu	099131 mus musculu	O9rla4 mus musculu	Q91z05 mus musculu	Q95m34 equus cabal	096pq8 homo sapien	0921k1 mus musculu	096qa6 homo sapien	Q91wt3 mus musculu	Ogbrv0 homo sapien	Q91wt1 mus musculu	091wrl mus musculu	096bb9 homo sapien	Q96dk0 homo sapien
		ID	Q9D8L4	099LC4	Q99L25	Q99L31	Q9R1A4	991205	Q95M34	Q96PQ8	Q921K1	Q96GA6	Q91WT3	Q9BRV0	Q91WT1	Q91WR1	Q96BB9	Q96DK0
		DB	11	11	11	11	11	11	9	4	Ξ	4	11	4	11	11	4	4
	Query	Length	473	463	473	468	437	473	337	701	278	614	481	200	481	488	597	496
æ	Query	Match	65.0	64.6	63.0	61.9	57.1	9.95	50.2	49.9	39.1	37.0	35.3	34.2	33.1	32.5	32.4	32,1
		Score	1636.5	1625.5	1585.5	1559	1436.5	1423.5	1263.5	1257	983	930.5	887.5	862	833.5	817	815.5	807
	Result	No.	н	7	3	4	S	9	7	80	6	10	11	12	13	14	15	16

Q9bul0 homo sapten	Q9bqb8 homo sapien	Q96aa6 homo sapien	Q991a6 mus musculu	Q96k68 homo sapien	Q96ey0 homo sapien	-	Q91wp5 mus musculu	Q91z07 mus musculu	Q91xel mus musculu		Q99m22 mus musculu	Q96kx8 homo sapien		Q9npp6 homo sapien		Q924p9 mus musculu	Q9y298 homo sapien		095978 homo sapien	-	096qs0 homo sapien	Q924q5 mus musculu	Q924r8 mus musculu	Q924p5 mus musculu	Q924q7 mus musculu	Q924r4 mus musculu	Q924q0 mus musculu	Q924p8 mus musculu
\$ 09BU10	\$ 09BQB8	1 Q96AA6	11 Q99LA6	\$ 096K68	1 Q96EY0			11 091207					11 Q9DCD9			11 Q924P9		11 092402	1 095978	11 Q924R3						11 Q924R4		
597	597	618	484	494	613			486	•								Ī	142	157	145	-				in	10	m	
30.4	30.3	30.0				28.9		27.9	27.5	26.2		25.6	24.0	23.1	21.4	21.0	20.9	20.4								19.4		19.3
765.5	761.5	755.5	755	737	735	727.5	721.5	703	692.5	629	655	644	605	580.5	539.5	527.5	525	514	511	510.5	499.5	495.5	494	493	492.5	488.5	486.5	486
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	4.0	41	42	43	44	45

## ALIGNMENTS

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61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120
                                                                                                                                                                                                                                                                                                                                                             61 GOGLEWMGEIDPSDSYTNYNOKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                                                      180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 RDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 ISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                       64.6%; Score 1625.5; DB 11; Length 463; 63.6%; Pred. No. 4.6e-128; ive 72; Mismatches 89; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
             InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 3.

SMART; SM00409; IG; 2.

SMART; SM00407; IGc; 2.

SMART; SM00406; IGv; 1.

SMART; SM00406; IG_liv; 1.

SMART; SM00290; IG_live; 1.

SROSTTE: PS002290; IG_MHC; UNKNOWN_1.

SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR003599; Ig.
Interpro: IPR003599; Ig.cl.
Interpro: IPR003600; Ig_like.
Interpro: IPR003006; Ig_MHC.
Interpro: IPR003506; Ig_V.
Pfam; PF00047; Ig; 4.
SMART: SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2001) to the
EMBL; BC003888; AAH03888.1;
HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                           Query Match 64.6%
Best Local Similarity 63.6%
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                             9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810066009 GENE.
                                                                                                                                                                                                                                                                                65.0%; Score 1636.5; DB 1:
63.7%; Pred. No. 5.6e-129;
Live 70; Mismatches 94;
                                                                                                                                                                                                       PS00290; IG_MHC; UNKNOWN_1
473 AA; 51699 MW; 9DED
         InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig_cl.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 3.
SMART; SM004106; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; 19.
InterPro; IPR003597; 19_c1.
InterPro; IPR003600; 19_like.
                                                                                                                                                                                                                                                                                                                      303; Conservative
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                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                         PROSITE; 1
SEQUENCE
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Best Local Si
Matches 303,
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099LC4;
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ID DTT DDT DDT RRA RRA DR RRA DDR DDR

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Length 468;

96352328B3332ADB CRC64;

51661 MW;

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Query Match 61.9%
Best Local Similarity 62.7%
Matches 296; Conservative
   468 AA;
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SEQUENCE
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                                                                                           Gaps
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                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                        178 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR
                                                                                                                                                                                                                                                                                                                            121 --YSNN-WYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                                                                                                                                                                                                                                                                                                                                                         EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 1585.5; DB 11; Length 473; 63.4%; Pred. No. 1.1e-124; Live 61; Mismatches 106; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
R HSSP; P01842; 7FB.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003509; Ig.
R InterPro; IPR003500; Ig_Alke.
R InterPro; IPR003506; Ig_MC.
R InterPro; IPR003506; Ig_W.
R SMART; SM00407; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 1.
R SMART; SM00410; IG_IIke; 1.
R SMART; SM00410; IG_IIke; 1.
R PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_LIKe; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 473 AA; 52449 MW; BE98899F986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                              Best Local Siminaricy Autohes 301; Conservative
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                                                                     Query Match
Best Local Similarity
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, 1st light and heavy chains) and construction of a
antibody (Mab 7, 1st light and heavy chains) and construction of a
antibody (Mab 7, 1st light and heavy chains) and construction of a
submitted (MaY 1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF152372; AAD40243.1; -.

R HSSP; P01842; 7FAB.

InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003506; Ig_MHC.

R FART; SM00447; Ig; 4.

R SMART; SM00410; IG_Like; 2.

R RART; SM00410; IG_Like; 2.

R RART; SM00410; IG_Like; 2.
                                                                                                                                                                                                                       YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                    237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
                                                  Gaps
                                                                                                                                                                                            GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                           WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
61.9%; Score 1559; DB 11;
62.7%; Pred. No. 1.8e-122;
iive 62; Mismatches 108;
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01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last seque
01-DEC-2001 (TrEMBLrel, 19, Last annol
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SSVFIFPPKPKDVLITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
                                                                                                                       21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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   DB 11; Length 437;
                                                              17;
                                                           96; Indels
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                            Pred. No. 3e-112;
57.1%; Score 1436.5;
59.3%; Pred. No. 3e-1
                                                        71; Mismatches
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12D 209
13D 209
14D 201
15D 209
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MEDLINE-983831416; PubMed-9717671;
MEDLINE-983831416; PubMed-9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c.mu, c.gamma, c.epsilon and c.alpha genes.";
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
              SISSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPI 240
                                                                  ALISGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD 244
                                                                                                         FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
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                                                     KT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Last sequence update)
Last annotation update)
CHAIN CONSTANT REGION
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                                                                                                                                                                                                                                                                                                             337
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                                                                                                                                                                                                                                                                                                                                                                                                                     Equus caballus (Horse).
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Query Match
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          240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK 299
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375 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK 432
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                              Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           cells and
                                                                                                                                                                                                                                                                    "Targeting tissue factor on tumor vascular endothelial cells an cells for immunotherapy in mouse models of prostatic cancer."; proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL; AF272774; AARS6868.1; -. SEQUENCE 701 AA; 77826 MW; 94ACGCEB42CC992F CRC64;
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Pred. No. 6.9e-97;
2; Mismatches 0; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC012207; AAH12207.1; -.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
                                           LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPGK 470
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MEDLINE-21477448; PubMed-11593034;
Hu Z., Garen A.;
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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nes 230; Conservative
                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                    Homo sapiens (Human).
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Q96PQ8;
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                                                                                                                                                                                       61 GQGLEWIGNINPNSGGTNYNEKFKNKATLAVDKSSSTVYMQLSSLTSEDSAVYYCTRGYG 120
                                                                                                                                                                                                                                                 XSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                         240
                                                                                                                                                                 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YSNNW--YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                           Gaps
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                                                                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                      180 WNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.0%; Score 930.5; DB 4; Length 614; 36.7%; Pred. No. 1.4e-69; ive 84; Mismatches 166; Indels 115;
                                           ..
6
Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---CDKTHTCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. STEF536E77AA9BBB CRC64; GTPOIRENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
  Score 983; DB 11;
Pred. No. 1.8e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                        RVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPRSR 275
                                                                                                                                                                                                                                                                                                                                                                                                                   241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Æ
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN (PROTEIN FOR MGC:15420).
                                        33;
  39.1%;
67.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.73
Matches 212; Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001
                                           Matches 186;
                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96GA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096GA6
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                    415
                                                                                          PSREEMT-KNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                    |:|: | :: || :| || || 416 SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQH-DSNPVQELNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                  35.3%; Score 887.5; DB 11; Length 481; 42.7%; Pred. No. 4.1e-66; Live 73; Mismatches 172; Indels 31;
                                                                                                                                                                                                                                                                                                                  TISSUE-COLON;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011488; AAH13488.1; -..
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.0 KDA PROTEIN.
                                                                                                                                   431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                                                                                                             481 AA
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.7%
Matches 206; Conservative
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                      Q91WT3;
01-DEC-2001
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                                                                                                                                                                        RESULT 11
Q91WT3
                                                                              376
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DYS---NNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK---------DTLM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPSQDVTV------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 ISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSTYRVVSVLIVLHQD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 862; DB 4; Length 500; 41.3%; Pred. No. 6e-64; Live 67; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; IMCP.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HOMPOSHETICAL 54.2 KDA PROTEIN.
                                                                                                                                                                                                              Ä.
                                                                                                                                                                                                              200
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SWART; SM00409; IG; 42.
SWART; SM00406; IGV; 1.
SWART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003597; 19_C1.
InterPro; IPR003600; 19_11ke.
InterPro; IPR003066; 19_MHC.
InterPro; IPR003596; 19_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 41.3
Matches 207; Conservative
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ig; 4.
9; IG; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00290; IG
Hypothetical protein.
SEQUENCE 500 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047
                                                            470
                                                                                                      463
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                                                                                               g.
                                                            469 GK
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                                                                                                                                                                                                                                       09BRV0
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18;

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Query Match
Best Local Simi
Matches 191;
                                                                     Q91WR1;
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Q96BB9
RESULT 14
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Q91WT1;
Q91DEC-2001 (TERBLrel. 19, Last sequence update)
01-DEC-2001 (TERBLrel. 19, Last annotation update)
01-DEC-2001 (TERBLrel. 19, Last annotation update)
01-DEC-2001 (TERBLrel. 19, Last annotation update)
Mus musculus (Mouse)
Mus musculus (Mouse)
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Musmmalia; Eutheria, Rodentia, Sciurognathi; Muridae; Musinae; Mus
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462 VGHEALPLAFTQETIDRLAGK 482
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Best Local Similarity 40.2%
Matches 194; Conservative
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121 YSNNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPE 175
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 53.0 KDA PROTEIN.
HYBOTHETICAL 53.0 KDA PROTEIN.
BURS muscalus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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488 AA; 52964 MW; F12068460B400B9D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
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IDRLSGK 470
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                                                                                                                                                                                                                                                                                                                            GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARN-R 119
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                                                                                                                                                                                                                                                           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                               231 N-----TKVDKRVEPKS------CDKTHTCP-----
                                                                                                                                                                                             Ouery Match 32.4%; Score 815.5; DB 4; Length 597; Best Local Similarity 32.6%; Pred. No. 6.2e-60; Matches 190; Conservative 94; Mismatches 179; Indels 119;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                             SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Search completed: August 14, 2002, 15:22:19 Job time: 687 sec

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August 14, 2002, 15:15:40; search time 230.21 Seconds (Without alignments) 226.770 Million cell updates/sec
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1 MGWSCIILFLVATATGVHSO......MHEALHNHYTOKSLSLSPGK 470
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
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                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
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3: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
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5: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
7: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
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13: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
14: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\*
15: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\*
16: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\*
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19: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
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20: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
21: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
22: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\*
22: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 

					SUMMARIES	
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	2518	100.0	470	21	AAW90936	ACES Designation
7	2498	99.2		19	AAW83037	Anti-Fas humanis
e	2498	99.2	470	21	AAB14779	Humanised anti-F
4	2498	99.2		21	AAW90929	Humanised HFE7A
S	2498	99.2		21	AAW90935	Humanised anti-F
9	2497	99.2		2	AAW90934	Humanised anti-F
7	2495	99.1		21	AAW90933	Humanised anti-F
8	2485	98.7		19	AAW83036	Anti-Fas humanis
6	2485	98.7		21	AAB14776	Humanised anti-F
10	2485	98.7		21	AAW90926	Humanised HFE7A
11	2363.5	93.9		22	AAM52156	Humanised HMFG-1

741 22 AAM52159 Humanised HMFG-1 h 729 22 AAM52159 Humanised HMFG-1 h 74 730 22 AAM52157 Humanised HMFG-1 h 74 74 22 AAM52160 Humanised HMFG-1 h 74 74 22 AAM52160 Humanised 323/A3 ( 8 652 19 AAM848650 Humanised 323/A3 ( 8 652 19 AAM848650 Humanised 323/A3 ( 8 652 19 AAM848650 Humanised 323/A3 ( 8 70 21 AAM88464 Chimeric anti-CD2 ( 9 476 20 AAM88464 Chimeric 2403 1gG ( 9 476 20 AAM831023 Chimeric 2403 1gG ( 9 476 14 AAR331023 Antibody D heavy c ( 9 479 14 AAR331023 Antibody D heavy c ( 9 470 14 AAR33102 Antibody D heavy c ( 9 470 14 AAR33102 Antibody D heavy c ( 9 470 14 AAR33102 Humanised anti-II- H	AAW90936 standard; Protein; 470 AA.  AAW90936 standard; Protein; 470 AA.  AAW90936;  08-AUG-2000 (first entry)  Humanised HFE7A designed heavy chain HHH type protein.  Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antimemetic; anti-Fas; nephrotropic; antilnfertility; neuroprotective; antiarteriosclerotic; hepatotropic; antimenated; apoptosis; systemic lupus erythematics.  Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myaathenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; misulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; qlomerulonephritis; hepatitis; transplant rejection.		Факр0307711	98JP-0276881. 98JP-0276882.
888 888 888 888 888 888 888 888 888 88	tandard; Prc  (first er  HFE7A desigr  ody; human;  glc; anti-an  ical; immun  ic; antinf  ic; numanize  ic; numanize  clascase; rhe  syndrome; ar  e syndrome	1 1	60-dabb	98JP-02 98JP-02
12 2363.5 14 2358.5 16 2352.5 17 2291.5 20 2228.5 21 2266.9 22 2228.9 23 222.5 24 222.8 25 223.8 26 223.8 27 223.8 28 223.8 28 223.8 29 2210.5 20 223.8 20 223.8 20 223.8 21 223.8 22 223.8 23 223.8 24 223.8 25 223.8 26 223.8 27 223.8 28 2210.5 28 28 28 28 28 28 28 28 28 28 28 28 28 2	AAM90936  ID AAW90936  XX  AAC AAW90936;  XX  XX  XX  XX  XX  XX  XX  XX  XX	Synthetic. EP990663-A2.	5-APR-2	0-SEP-1998 0-SEP-1998

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allerial, immunosuppressive, thyromimetic, antiarteriosclerotic, antinfartility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthitis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, thrombopenia gravis, another disease, autoimmune hemolytic anemia, sterility, myssthenia gravis, another disease, antiamune hemolytic anemia, sterility, myssthenia gravis, another disease, antiamune hemolytic anemia, sterility, myssthenia gravis, antipher sclerosis, Basedow's disease, thrombopenia purpura, insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fullinant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mind the native ligand, do not induce liver disease, and have reduced risk of a human anti-nurine antibody response. This sequence represents a humanised anti-Fas antibody HFF7A heavy chain construct HHH type
                                                                                                                                                              New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                             Tamaki I, Takahashi T;
                             Nakahara K,
                                                                                                                                                                                                                                                                              Claim 2; Page 188-189; 263pp; English.
                             Haruyama H,
                                                                            WPI; 2000-258930/23.
                                                                                                            N-PSDB; AAA11655
                             Serizawa N,
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Gaps ; 0 Length 470; 0; Indels Score 2518; DB 21; Pred. No. 1.4e-144; 100.0%; Scor. 100.0%; Pred. No. 1... 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 470; Conservative

470 AA;

Sequence

1 mgwsciilflvatatgvhsqvqlvqsgaevkkpgasvkvsckasgytftsywmqwvrqap 60 1 MGWSCIILFLVATATGVHSOVOLVOSGAEVKKPGASVKVSCKASGYTFTSYWMOWVROAP

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61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120

121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180

WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240 181 g á

241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 ò a

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YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 301 301 ò g

KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV

361

à

420

361 kakgqprepqvytlppsreemtkngvsltclvkgfypsdiavewesngqpennykttppv 420 421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470 a ò

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AAW83037

KW apoptosis; HFE7A; autoimmune disease; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; KW systemic lupus erythematosus; graft versus host disease; KW syofaroms; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; W rheumatoid arthritis; autoimmune haemolytic anaemia; W myasthenia gravis; multiple sclerosis; Basedow's disease; W thrombopenia purpura; insulin-dependent diabetes; allergy; W atopy; arteriosclerosis; myocarditis; cardiomyopathy; W glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy. Anti-Fas humanised antibody HFE7A heavy chain. AAW83037 standard; Protein; 470 AA. 15-MAR-1999 (first entry) AAW83037; A COOR ON A COOR

..19 label= Sig\_peptide Location/Qualiflers Synthetic. Peptide

Homo sapiens.

20..470 /label- Mat\_protein 20..140 /label= variable /label= Constant "claim 9" 50..54 /label= CDR\_H1 .464 /note= Protein Region Region Region

/note= "claim 9" 118..129 /note= "claim 9" /label= CDR\_H2 /label= CDR\_H3 Region Region

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AU9859701-A.

08-OCT-1998

98AU-0059701 30-MAR-1998; 97JP-0276064 97JP-0082953 97JP-0169088 08-OCT-1997; 25-JUN-1997; 01-APR-1997

(SANY ) SANKYO CO LTD.

Jun O, Kimihisa I; , Tohru T; Hideyuki H, Hiroko Y, Jı O, Nobufusa S, Shin Y, Masahiko O, Akio S,

WPI; 1998-543440/47. N-PSDB; AAV70080. New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS

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24-NOV-2000 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 yvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, anyocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                     green conserved in the human IgG heavy chain. Host Escherichia colipgipply SAMK 70298 harbors plasmid pgHPDHY3 carrying a fusion fragment of the humanised HV type HFZA heavy chain and DNA encoding human IgG1 constant region (see AAY7088), and is deposited as FERM BP-6273 (claimed). The invention provides methods for producing humanised antibodies by culluring host cells. Humanised versions of HFZPA (see AAW83031.37), like native HFZPA, are capable of inducing apoptosis in abnormal cells expressing Fas, and of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                             This is the amino acid sequence of the HV type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. It includes humanising R44G and A76T amino acid substitutions that are are conserved in the human IgG heavy chain. Host Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                              inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to
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Pred. No. 2.3e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
             Claim 22; Page 225-227; 292pp; English.
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Best Local Similarity
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                                                              Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
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                                Humanised anti-Fas antibody heavy chain, SEQ ID NO:117
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Pred. No. 2.3e-143;
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- Homo sapiens.
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Best Local Similarity
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Chimeric
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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunoadulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sollerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule (1) that, induces apoptosis in cells with a abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-inflammatory, immunomodulatory, dermatological, immunosuppressive, thyromimetic, anti-inflammatory cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases associated with the Fas/Fas ligand system, especially systemic
241 kscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
                                    420
                                                                                                                                     361 KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised HFE7A designed heavy chain protein #2.
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                versus host disease, Sjorgen's syndrome, pernicious or hypopiastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEFTA designed heavy chain which is used in the method described in the invention.
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Best Local Similarity 98.9
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This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Eas antidiabetic, anti-antiatic, antiviral, inmunomodulatory, dermatological, immunosuppressive, thyromimetic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirineumatic, nephrotropic, antilnfertility, neuroprotective, antirheumatic, nephrotropic, antilnfertility, neuroprotective, antilnfertilosed Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive alsaying to a fas/Fas ligand system, especially systemic disease, solorated syndrome, competities, and sale syndrome, conditions or hypoplastic versus host disease, soloraderma, scerility, myasthenia gravis, anemia, Addison's disease, scleroderma, Scerility, myasthenia gravis, anemia, Addison's disease, thrombopenia purpura, insulin confident diabetes mellitus, allergy, arteriosclerosis, myocacidis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody reaponse. This sequence represents a humanised anti-marine disease. This sequence represents a humanised anti-marine disease.
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Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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Pred. No. 2.3e-143;
3; Mismatches 2;
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anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotrophc; antilnferthlity; neuroprotective; antiarteriosclarotic; hepatotrophc; humanized; apoptosis; systemcic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardlomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                            301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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Humanised anti-Fas designed heavy chain Heu 1 protein.

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apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antinifertility, neuroprotective, antirheumatic, nephrotropic, antinifertility, neuroprotective, antistensoclerotic, cardiant and hepatropic activity. (I) induce apotation of ligand to call surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Corbn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, antitice, and all and a
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470 AA; Seguence

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                                                                                                                                                                         121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                              Gaps
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99.2%; Score 2497; DB 21; Length 470; 98.9%; Pred. No. 2.6e-143;
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AAW90933 standard; Protein; 470

AAW90933

(first entry)

08-AUG-2000

AAW90933;

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This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas (1 igand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, anti-heumatic, nephrotropical, immunosuppressive, thyromimetic, anti-heumatic, nephrotropical, immunosuppressive, thyromimetic, anti-heumatic, nephrotropic, antidifertility, neuroprotective, anti-heumatic, nephrotropic, antidifertility, neuroprotective, contining to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent consenses associated with the Fas/Fas ligand system, especially systemic specials with the Fas/Fas ligand system, especially systemic consenses associated with the Fas/Fas ligand system, especially systemic consenses, sjorgen's syndrome, pernicious or hypoplastic versus host disease, soleroderm's Goodpasture syndrome, Conh's disease, autoimmune hemolytic anemia, sterility myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, is cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, is unhibit apptoss in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic contine disease models. (I) act on the active site of Fas, i.e. they minic is described anti-enalibody reavy chain construct designated Heu I with the method of the invention.
                                      Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepartotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple solerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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Best Local Similarity 98.7%; Pred. No. 3.5e-143;
Matches 464; Conservative 4; Mismatches 2;
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                                                                                                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                   361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                               GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                121 ysnnwyfdvwgqgtlvtvssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvs 180
       MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                              HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                   myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                              Anti-Fas humanised antibody HFE7A heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Mat_protein
                                                                                                                                                                                                                                                                                             AAW83036 standard; Protein; 470 AA.
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/label- CDR_H2
/note= "claim 9"
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|abel= Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFB7A. E. coll pyELTA62 SANK 7397 harbors plasmid pyERSTA62 carrying a fusion fragment of the humanised VD type HFB7A heavy chain and DNA encoding human IgGl constant region (see AAV70079), and is deposited as FERM BP-6074 (Claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFB7A (see AAW83031-37), like native HFB7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of antibodies are used to evaluate, in animal models, treatments of antibodies are used to evaluate, in animal models, treatments of alseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, sleroderma, Sjoren syndrome, Crohn's disease, thromatoid arthritis, autoimmune heamolytic anaemia, Sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thromatopenia purpura and insulin-dependent diabeters), allengies, aropy, arteriosclerosis, multiple sclerosis, Basedow's disease, thromatograftis, nyopolastic myocarditis, cardiomyopathy, glomecular nephritis, hypoplastic maemia, hepatitis, AIDS and transplant rejection (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate druys in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimihisa I;
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s, Shin Y, Tohru T;
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                          /label= CDR_H3
/note= "claim 9"
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98.5%;
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97JP-0169088.
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118..129
/label=_C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hideyuki H,
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                                                                                                                                                                                                                                                 30-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masahiko O,
                                                                                                                     AU9859701-A
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autofimmune diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                      420
 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                   360
                                                                                                                                     361 KAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV 420
                                                                                      YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                     LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
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                                                                                                                                                                                                                                                                                                                          AAB14776 standard; Protein; 470
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Chimeric - Homo sapiens
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N-PSDB; AAA72159.
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                                                                                                                                300
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                             Gaps
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                                                                      antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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 Length 470;
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 Score 2485; DB 21;
Pred. No. 1.4e-142;
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                            Mismatches
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                            Conservative
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              Similarity
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                            463;
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  Query Match
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into the control of that, induces apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an open by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-aremic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, artirateriosolerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cells usrface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic versus host disease, soleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, allergy, almerulonephritis, hepatitis (fulminant, chronic, viral Gependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B. C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic murine disease models. (I) act on the active site of Fas, i.e. they minic inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEPA designed heavy chain which is used in the method described in the invention.
                                                                                                                                                               New humanized anti-Fas antibody, useful for treating or preventing e. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like
                             Takahashi T;
                                                                                                                                                                                                                                                                          Example reference 15; Page 134-136; 263pp; English.
                             Tamaki I,
                                                                                                                                                                                                                           cells with abnormal Fas-Fas ligand systems
                             Nakahara K,
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                             Нагиуаша
                                                                               WPI; 2000-258930/23
                                                                                                             N-PSDB; AAA11597
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                             Serizawa
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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240

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KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                 Humanised monoclonal antibody; polymorphic epithelial mucin; PEMI;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                                                                                         Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
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93.6%; Pred. No. 5.1e-135;
ive 19; Mismatches 8;
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                         AAM52156 standard; Protein; 731
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02-OCT-2000; 2000US-237159P.
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                                                                                 (first entry)
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Matches 440;
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358 kakgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppv 417
 61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                           121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                      241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                  WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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ID AAM52158 standard; Protein; 729
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                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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238 kscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297
                                                                                           301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                           361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
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93.6%; Pred. No. 5.1e-135;
ive 19; Mismatches 8;
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02-OCT-2000; 2000US-237159P
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Synthetic.
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monoclonal antibody; polymorphic epithelial mucin; PEM1; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                               Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
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                                                                                     cytotoxic; endonuclease; DNase
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Query Match

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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA025682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
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cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                                                               DB 22;
                                                                              93.7%; Score 2358.5; DB 93.6%; Pred. No. 1e-134; iive 19; Mismatches
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                                                                     Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity f polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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No. 1e-134;
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93.68;
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                                 2001-662969/76
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                                                                                                                                                                                                                                                                                            cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytoctoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                      invention relates to a compound which comprises a target
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                                                                                                                                                                                                                                                                                                                                                                                                                  93.4%; Score 2352.5; DB 22
93.6%; Pred. No. 2.3e-134;
iive 19; Mismatches 8;
                                                                                                                                                                                                                                                              Claim 20; Figure 8; 176pp; English.
                                                                                           2000GB-0008049
2000US-237159P
                                                                     26-MAR-2001; 2001WO-GB01324
                                                                                                                               LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.4
Best Local Similarity 93.6
Matches 438; Conservative
                                                                                                                               (ANTI-) ANTISOMA RES
                                                                                                                                                                             WPI; 2001-662969/76
                                                                                                                                                                                                                                                                                                                                                                                  730 AA;
                      WO200174905-A1
                                                                                           03-APR-2000;
02-OCT-2000;
                                             11-OCT-2001.
 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Sequence

23, Appl 24, Appl 23, Appl 23, Appl 31, Appl 4, Appl 17, Appl 17, Appl 17, Appl 112, Appl 4, Appl 4, Appl 5, Appl 12, Appl 2, Appl 2, Appl 2, Appl 2, Appl 2, Appl 2, Appl 3, Appl 3, Appl 4, Appl 3, Appl 3, Appl 4, Appl 12, Appl 4, Appl 5, Appl 6, Appl 6, Appl 6, Appl 6, Appl 6, Appl 7, Appl 7, Appl 8, Appl 8,

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US-08-157-101A-7
PCT-US93-07832-23
US-07-916-0848-45
US-08-437-642B-23
US-08-437-642B-23
US-09-247-352-3
US-08-437-56B-17
US-08-341-56B-17
US-08-341-56B-17
US-08-441-7
US-08-461-56B-17
US-08-461-56B-17
US-08-461-968A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CFOWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERNST & KURZ
N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CIASTBETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30, 377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET STAIRTEENTH ST. N. CITY: WASHINGTON STATE: D. C. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
    ; MOLECULE TYPE: protein US-08-378-939-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 71, 3 sequence 71, 5 sequence 67, 8 sequence 90, 8 sequence 22, 8 sequence 12, 8 sequence 14, 8 sequence 14, 8 sequence 16, 8 sequence 16, 8 sequence 18, 8 sequen
                                                                                                                                                                                                                                                                                               1 MGWSCIILFLVATATGVHSQ.......MHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                            Search time 82.88 Seconds
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1: /cgn2_6/ptodatu2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatu2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatu2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodatu2/iaa/PcTUS_COMB.pep:*
                       4.5
Compugen Ltd
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US-08-458-516-13

US-09-025-985-71

US-09-025-985-71

US-09-026-985-71

US-09-026-985-71

US-09-048-7378-67

US-09-485-7378-67

US-08-793-450-8

US-08-793-450-8

US-08-137-622

US-08-137-622

US-08-887-3528-14

US-08-109-207C-14

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-16

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                       GenCore version (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 protein search, using sw mode]
                                                                                                                                                          August 14, 2002, 15:17:08
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Gapop 10.0 , Gapext 0.5
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Maximum |
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Gaps

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us-09-499-662-157.rai

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                                                                                                                                                                                                                                                                     SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                                                                                                                          NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379
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                                                                                                                                 9
                                                                                                            299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                        20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY
                                                                                                                                                                                                                                                                                                                                                           SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG
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                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INPORMATION:
GONZALEZ, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
  Length 449;
                                            Indels
88.6%; Score 2230; DB 1;
93.1%; Pred. No. 2.2e-162;
iive 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windpatin (Genentech)
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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20-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DAYS:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
FRIGH APPLICATION DATE: 40/038,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                              Matches 420; Conservative
  Query Match
Best Local Similarity
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ZIP: 94080
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TOPOLOGY: Linear
                                                                                                                                                                                                                                                                              Similarity
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APPLICANT: Hillman
                                                                                                                                                                                                                               US-09-026-985-71
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                                                                                                                                                                                                                                                                  Query Match
Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 71, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Genzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             Length 452;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                             DB 3;
                                                                                                                                                                                          87.8%; Score 2210.5; DB 3; 90.3%; Pred. No. 6.9e-161; ive 27; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/POCKET NUMBER: P108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-530
TELEFAX: 650/952-9881
                                                                                           INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
FILING DATE: 21-Feb-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   Best Local Similarity 90.3
Matches 408; Conservative
                                                                                                                                           TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                       US-09-027-449-71
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                                                                                                                                                                                           Query Match
Best Local S
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121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2210.5; DB 4
Pred. No. 6.9e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
                                                                                                                                                                                                                     P1085R3-1
                                                                                APPLICATION NUMBER: US/09/026,985 FILING DATE: 20-Feb-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 8, Application US/09049672A
; Patent No. 6135941
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: LOVG, R.Chard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-5530
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Que, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMI
                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillman, Jennifer
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424 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                              Sequence 67, Application US/09485737B Patent No. 6350860
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                                                                                                                                                                                                                                                                                                                      PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: SYNTHETIC US-09-485-7378-67
                                                                                                             GENERAL INFORMATION:
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US-09-485-737B-90
                                                                  US-09-485-737B-67
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Pate
SEQ ID NO 67
LENGTH: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 2207.5; DB 4
; Pred. No. 1.2e-160;
20; Mismatches 27;
                                                                                                                                     SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
                          E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                      PF-0497
                                                                                                                                                                                                                                                                                        NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.78;
89.28;
                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 89.2
Matches 414; Conservative
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
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Best Local Similarity
                                                     Palo Alto
                                                                                 USA
                          ADDRESSEE:
                                                                 STATE: C
                                        STREET:
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APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 THTCPPCPAPELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 IILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 YEDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 LISGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.3%; Score 2172; DB 4; Best Local Similarity 88.0%; Pred. No. 6.2e-158; Matches 409; Conservative 20; Mismatches 32;
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61 GOGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2146; DB 4; Leus-
pred. No. 6e-156;
                                                                                                         ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                           E: P.C.
1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.2%; Scolumes 85.3%; Pred. No. bell. 185.3%; Pred. No. bell. 185.3%; Mismatches 15; Mismatches 185.3%; Mis
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                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                             STREET: 1755 SOU
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                             22202
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
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                                                    APPLICANT: BUYSE, Marie-Ange
APPLICANT: BAYSE, Marie-Ange
APPLICANT: BUYSE, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISBASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
FRIOR APPLICATION NUMBER: PCT/PP 98/05165
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 YFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMGEIDPSDSYTNYNQKFKGRVTITRDTSTAYMELSSLRSEDTAVYYCARNRDYSNNW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THICPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGV 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-793-450-8
Sequence 8, Application US/08793450
Sequence 8, Application US/08793450
Sequence 8, English Color 
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88.0%; Pred. No. 1.1e-157;
iive 20; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: SYNTHETIC US-09-485-7378-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.09
Matches 409; Conservative
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LENGTH: 711
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80 NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.1%; Score 2142.5; DB 3; Best Local Similarity 88.3%; Pred. No. 1.1e-155; Matches 401; Conservative 20; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                     437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                               421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P0709P2C1
                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08437642B Patent No. 6054297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEDHONE: 650/225-1994
TELEFAX: 650/352-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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Amino Acid
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US-08-437-642B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.1%; Score 2142.5; DB 2; Length 454; 88.3%; Pred. No. 1.1e-155;
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                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1.84 PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINDATIN (Genethech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
TITLE OF INVENTION: Immunoglobulin Variants
OURRESPONDENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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                                                                                  Sequence 22, Application US/07934373C Patent No. 5821337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0705
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1994
TELEPHONE: 650/252-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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Amino Acid
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Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                              California
: USA
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
                                                         US-07-934-373C-22
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
                                                                                                                                                                                                                                                          LQSSGLYSLSSVVTVPSSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
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                                                                                                                                                                                                                                                                                                                                                                                              LIGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                       20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                         DB 5; Length 454;
                                                                                      Indels
                                                    Query Match 85.1%; Score 2142.5; DB 5; Best Local Similarity 88.3%; Pred. No. 1.1e-155; Matches 401; Conservative 20; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PI.
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TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: Genenteck STREET: 1 DNA Way
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     PCT-US93-07832-22
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, 4221

Sequence 22, 4221

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITX: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                             437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/US92/05126
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 709P2PCT TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US93-07832-22
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TOPOLOGY:
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TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
 TELECOMMUNICATION INFORMATION:
                                                                                                                                 US-08-887-352B-16
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US-08-466-151-65
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                      ;
                                                                                                                                                                                                                                                                       110 SSASTKGPSVFPIAPSSKSTSGGTAALGCLVKDYFPEPVTVSRNSGALTSGVHTFPAVLQ 179
                                                                                                                                                                                                                                                                                                                                                                                                            240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 YNQKFKGRVTITRDISTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTV 138
                                                                                                                                                                                                                                                                                                                        SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                         199 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                      Gaps
                                                                                                                                                                                                       20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                   Length 451;
                                                                                                                                                     Indels
                                                                                                                 85.0%; Score 2141; DB 2;
88.3%; Pred. No. 1.4e-155;
iive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Winpatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/887,3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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03-Jul-1997
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Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Svoboda. Craig G.
RECISTRATION NUMBER: 39,044
REPERENCE/DOCKET NUMBER: 91123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
STATE: California
COUNTRY: USA
              LENGTH: 451 amino acids TYPE: Amino Acid
                                                                                                                                                   Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                  Linear
                                                                                                                 Query Match
Best Local Similarity
Matches 399; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94080
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TOPOLOGY:
US-08-887-352B-14
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US-08-887-352B-16
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240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                       20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                              180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                        SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
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                                           3
    Length 451;
                                           Indels
85.0%; Score 2141; DB 2;
88.3%; Pred. No. 1.4e-155;
tive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/08466151 Patent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
Query Match 85.0%
Best Local Similarity 88.3%
Matches 399; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Gaps

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Indels

Length 451;

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240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                                                                                                                                                                                                                                                                               79 YNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTV 138
                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                                                                                                                                                                                                   SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                  ; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-109-207C-14
                                                                                                                                                                                                                                                                               85.0%; Score 2141; DB 4;
88.3%; Pred. No. 1.4e-155;
iive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 14, 2002, 15:17:09
Job time: 692 sec
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.39
Matches 399; Conservative
                                                                                                                                                                               NAME/KEY: Artificial LOCATION: 1-451
                                                                                                                                                  ORGANISM: Artificial
                                                                                                                                   TYPE: PRT
                                                                                                                                                                  FEATURE:
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 SSASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%; Score 2141; DB 3;
88.3%; Pred. No. 1.4e-155;
iive 23; Mismatches 28;
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                                                                                                                                                      FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craiq G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-109-207C-14
Sequence 14, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
TITLE OF INVENTION: Improved Anti-IC
          APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
                                                                                             APPLICATION NUMBER: 08/185899
FILING DATE: 25-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
                                                                                                                                                                                                                                           NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0716
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 399; Conservative
                                                               FILING DATE: 15-MAR-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:19:02; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

Title: Perfect score:

US-09-499-662-157 2518 1 MGWSCIILFLVATATGVHSO.......WHEALHNHYTQKSLSLSPGK 470 Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_71:\* Database

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Iq qamma-1 chain C	gamma-3				Ig gamma-2a chain	Ig gamma-2b chain		Ig heavy chain pre			Ig heavy chain V r	Ċ	Iq qamma 2a chain	gamma 2b	gamma-	gamma								gamma-3	Iq qamma-1 chain C	0	gamma-1 c	Ig gamma-3 chain C
er er	Синп	A23511	A60764	GZHU	G4HU	S37483	G2MS11	S40295	S22080	S01321	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	GIMS	PS0018	GIMSM	G3MSM
DB	Н	~	~	Н	Н	7	-	~	N	7	N	7	~	7	ď	4	~	~	П	~	٦	7	1	~	П	-	N	Н	Н
Length	330	377	377	326	327	469	474	446	470	475	472	374	444	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
% Query Match	69.8	S	65.0	63.9	63.5	63.2	61.0	9.09	59.0	58.9	58.8	57.3	57.2	50.3	50.1	49.8	49.4	49.0	48.9	48.9		•	45.9	•		45.5	45.5	45.3	45.2
Score	1758	1639.5	1637.5	1610	1599.5	1591.5	1535	1525	1485	1482.5	1481	1443	1440.5	1267	1261	1253	1245		1231.5	1231	$^{\circ}$	1165.5	1157	1155	1150	1145	1144.5	1140	1139
Result No.	н	7	Э	4	S	9	7	<b>&amp;</b>	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A. Contents: Eu A. Accession: A90564 A. Molecule type: protein A. Rote: this sequence the Glm(non-1) markers, 239-Glu and 241-Met A. Note: this sequence as the Glm(non-1) markers, 239-Glu and 241-Met R. Ponstingl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A. Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Ni

Ig gamma-2a chain	Ig gamma-2c chain Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
GZMSA	S0084/ G2MSAB	GZMSAM	PS0019	S06611	G2MSBM	147162	538864	S14683	S04845	S69131	S38950	A49444	S69340	B46529
	7 -	Н	7	~	Н	~	~	~	7	~	~	7	~	~
330	335	399	322	327	405	277	548	627	549	241	246	220	249	572
44.8	44.8	44.6	44.3	43.4	42.9	42.5	40.1	37.8	36.8	34.7	33.0	31.7	30.8	30.8
1129	1126.5	1124	1115	1093.5	1080	1070	1010	951	925.5	872.5	832	797	776.5	776.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1
_	GHHU
-	Ig gamma-1 chain C region - human
	C;Species: Homo sapiens (man)
_	C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
_	C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
	R; Ellison, J.W.; Berson, B.J.; Hood, L.E.
_	Nucleic Acids Res. 10, 4071-4079, 1982
-	A, Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
_	A; Reference number: A93433; MUID:82274238
	A;Accession: A93433
	A; Molecule type: DNA
	A; Residues: 1-330 <ell></ell>
	A; Cross-references: EMBL: Z17370
_	A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) mark∋r
_	A;Note: Lys-330 is removed after translation
_	R; Harris, L.J.
	submitted to the EMBL Data Library, October 1992
	A; Reference number: S33904
_	A; Accession: S36861
	A:Molecule type: DNA
	A:Residues: 2-330 <har></har>
	A.Cross-references: EMBL: 217370
_	R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
	Cell 29, 671-679, 1982
	A, Title: Structure of human immunoglobulin gamma genes: implications for evolution of
	A; Reference number: S33887; MUID:83001943
	A; Accession: S33887
	A; Molecule type: DNA
-	A; Residues: 88-113; 235-330 <tak></tak>
_	A; Cross-references: EMBL: Z17370
	R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
	Biochemistry 9, 3161-3170, 1970
	A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
_	A; Reference number: A90563; MUID:71064024
	A;Contents: myeloma protein Eu
	A; Accession: B90563
	A; Molecule type: protein
	A; Residues: 1-96,'R', 98-135 <cun></cun>
-	A; Note: this sequence has the Glm(3) marker, 97-Arg
	R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
_	Biochemistry 9, 3171-3181, 1970
	A, Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
_	A; Reference number: A90564; MUID:71064025
-	, CO

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gene:
                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       u) with an IGHG4
                                                                                                                                                                         C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                           Til gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Homo sapiens (man)
C.Bate: 14 May-1993 #Sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Bate: 14 May-1993 #Sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Bate: 14 May-1993 #Sequence N.P.
Immunogenetics 30, 250-257, 1989
A.Fitle: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an A.Fitle: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an immunoglobulin IGHG3 with a immunoglobulin IGHG3 w
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A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A;Moleoule type: DNA
A;Residues: 1-377 <4HC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.1%; Score 1639.5; DB 82.8%; Pred. No. 9.9e-87; iive 7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
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Matches 312; Conservative
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                                                                                                 A; Residues: 1-34, 'Q', 36-96,'K', 98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A; Residues: 1-34, 'Q',36-96,'K', 98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A; Nolecule types sequence has the Gim(1) and Gim(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschman, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Prinaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A; Teference number: A91723; MUD: 83289131 sierbaren monoklonalen Immunglobulins IgG1 KOL
A; Contents: myeloma protein KOL; disulfide bonds
A; Contents: myeloma protein KOL; disulfide bonds
A; Molecule type: protein
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Nolecule type: protein
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',1240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',1240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',1240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Title: The covalent structure of human gammaG-immunoglobulin. X. Intrachain disulfide
A; Reference number: A90565; MUD: 71064027
A; Contents: annotation; disulfide bonds
A; Reference number: A91667; MUD: 77070267
A; Contents: annotation; disulfide bonds
A; Reference number: annotation; disulfide bonds
A; Reference number: A91667; MUD: 77070267
A; Contents: annotation; disulfide bonds
A; Reference number: A91667; MUD: 77070267
A; Contents: annotation; disulfide bonds
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A.Gross-references: GDB:120085; OMIM:147100
A.Gross-references: 99/1; 114/1; 224/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and igav, the subunits associate into la C.Superfamily: immunoglobulin C region; immunoglobulin homology <IMI>
F.130-85/Domain: immunoglobulin homology <IMI>
F.243-310/Domain: immunoglobulin homology <IMI>
F.243-310/Domain: immunoglobulin homology <IMI>
F.243-310/Domain: immunoglobulin homology <IMI>
F.243-310/Domain: immunoglobulin homology <IMI>
F.137-206/Domain: immunoglobulin homology <IMI>
F.137-206/Domain: immunoglobulin homology <IMI>
F.137-210410/Ide bonds: interchain (to light chain) #status experimental
F.109/112/Disulfide bonds: interchain (to heavy chain) #status experimental
F.180/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 1.5e-93;
3; Mismatches 0;
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A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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Best Local Similarity 99.1%;
Matches 327; Conservative
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A Map position: 14932.33-14932.33
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C; Complex: An immunoglobulin cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology < Im2>
F; 239-306/Domain: immunoglobulin homology < Im2>
F; 239-306/Domain: immunoglobulin homology < Im3>
F; 27-33,140-200,246-304/Disulfide bonds: isstatus experimental
F; 27-83,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                        residues 25, 59, 60, and 264-268 that shown in having 60-Ala and in the ami
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C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
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                                                                                                                                                                                                                                                               Rimilstein, C.; Frangione, B.
Blochem. J. 121, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A90253; MUDE:72033500
A; Contents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MUID:69064124
A; Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.1e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.9%; SCu. 91.8%; Pred. No. 4...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                             A;Contents: annotation; Zie, revisions to A;Note: the revised sequence differs from
  number: A93132; MUID:80114419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   March 1980
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Matches 303; Conservative
                                                                                                                                                                      A; Reference number: A94591
                                                                         A; Molecule type: protein
A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, M.
                                                A; Accession: A93132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
     A; Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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A; Molecule type: DNA
A; Residues: 1-256 CELL>
A; Cross-references: GB: V00554; GB: J000230; NID: 932759; PIDN: CAB58438.1; PID: 96066056
A; Molecule type: DNA
A; Robady, A.C.; Tung, E.; Pudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A; Reference number: A92809; MUID: 81007873
A; Contents: myeloma protein Til
A; Accession: A92809
A; Molecule type: protein
A; Residues: 1-19; 0', 21-57, 2', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Molecule type: protein
A; Residues: 1-19; 0', 27, 758-767, 1979
A; Note: Trp-156 is at or near the comptement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem: S7, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Accession: A90752; MUID: 80001357
A; Accession: A90752
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A; Molecule type: protein
A; Residues: 1-24, E, 26-57, EV, 60-85;132-171, 222',175, B',177-193, D',195-196, Q',198-A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, 222', 175, B', 177-193, D',195-196, Q',198-A; Note: this sequence has since been revised
B; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain
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C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Ttle: Linkage and sequence homology of two human immunoglobulin gamma hee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV------ 238
                                                                                                                                                                                                                                                                                                                 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 393
                                                                                                                                                                                                                    Gaps
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                                                                                                                                             47;
                                                                                             Length 377;
                                                                                                                                             11; Indels
                                                                                          Score 1637.5; DB 2;
Pred. No. 1.3e-86;
7; Mismatches 11;
C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology
                                                                                          65.0%;
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                                                                                                                      Similarity
                                                                                             Query Match
                                                                                                                      Local
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A; Molecule type: mRNA
A; Residues: 1-469 <DUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 276-345/Domain: immunoglobulin homology <IMM>
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    A;Status: preliminary
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Best Local Simi
Matches 299;
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A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85, Domain: immunoglobulin homology <IM1>
                                                                                                                                                       A) Note: the sequence was determined from the germline gene
R) Pink, J.R.L., Buttery, S.H.; De Vries, G.M.; Milstein, C.
Blochem, J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S3488
R;Ducancel, F.F.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                immunoglobulin C-gamma4 gene.
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A;Reference number: S37483
A;Accession: S37483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%; Score 1599.5; 91.8%; Pred. No. 1.6e
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A; Residues: 1-30; 81-326 <PIN>
C; Genetics:
A; Gene: GDB:1GHG4
A; Cross-references: GDB:119340; OMIM:147130
R;Ellison, J.; Buxbaum, J.; Hood, L.
Mhal, J.1-18, 1981
A;Title: Nuclectide sequence of a human in
A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 91.8
Matches 303; Conservative
                                                                                                                A; Molecule type: DNA
A; Residues: 1-327 <ELL>
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                                                                                                                                                                                                                                                                                  A; Accession: A90249
                                                                                             A; Accession: A90933
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Cispecies: Mus musculus (house mouse)
Cibate: 31 Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
Cibate: 31 Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
CiAccession: S25057; A26135; A26235; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TWV) inactivating neotop specifi A;Reference number: S25057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                          358
                                                                                                                                                                              61 GOGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                    121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
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                                                                                                                               9
                                                Gaps
                                                                                                               180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSYTVTSSTWPSQSITCNVAHPASSTKVDKKIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                          181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                Indels
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Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A; Cross-references: GB:000461
A; Note: the sequence was determined from the germline g R; Tucker, PW: Marcu' K.B.; Slightom, J.L.; Blattner, Science 206, 1299-1303, 1979
    DB 2;
                                              Conservative 63; Mismatches 105;
63.2%; Score 1591.5; D
63.3%; Pred. No. 7e-84;
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C, Accession: S40293
C, Accession: S40293
R; Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.,
submitted to the EMBL Data Library, January 1993
A; Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A; Reference number: S40295
A; Accession: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
E; 1-446/Product: Ig gamma-za chain #status experimental <MAT>
E; 1-117/Domain: V-J- region <CHR>
F; 118-244/Domain: C region <CHR>
F; 118-244/Domain: C region <CHR>
F; 118-244/Domain: C region <CHR>
F; 215-230/Region: hinge
F; 231-340/Domain: C3 region <CH2>
F; 341-446/Domain: C3 region <CH2>
F; 341-446/Domain: C3 region <CH2>
F; 341-446/Domain: C3 region <CH2>
F; 360-427/Domain: immunoglobulin homology <IMM>
F; 220-441-199, 261-321, 367-425/Disulfide bonds: #status predicted
F; 22-96, 144-199, 261-321, 367-425/Disulfide bonds: interchain #status predicted
F; 224, 227, 229/Disulfide bonds: interchain #status predicted
F; 224, 227, 229/Disulfide bonds: interchain #status predicted
F; 224, 227, 229/Disulfide bonds: interchain #status predicted
F; 227/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Mus musculus (house mouse)
C.Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
   80 NOKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPEL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                             414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                   PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
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63.3%; Pred. No. 4.2e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus /house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                          A Accession 1.842.9.

A Maccession 1.862.9.

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       untranslated regions of the murine gamma2b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| ||:|||||||:|| ||:|| ||:|| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| 
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A; Title: Structure of the constant and 3' A; Reference number: A26235; MUID:80081501
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288; Conservative
                                                                                                           A; Accession: A26235
                                                                            A; Contents: MPC 11
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Best Local Si
Matches 288;
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419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Best Local Similarity 59.5%
Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                 A; Accession: S01321
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                                                                                                                                                                                               Igheavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: $22080; $06610; A31303
R;Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A;Reference number: $22080
A;Retaus: preliminary
A;Accession: $22080
A;Status: preliminary
A;Molecule Lype: mRNA
A;Residues: 1-470 < SANN
A;Residues: 1-470 < SANN
A;Residues: 1-470 < SANN
A;Residues: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
A;Reference number: $06610; MUID:90097956
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C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNR--D 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 WT--LLFVLSAPIGVLSQVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGK 62
EEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 142-470 <SYM>
A; Cross-references: EMBL:X16701
C; Genetics:
                                                                                 Query Match
Best Local Similarity 60.69
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CH gamma-1
98/1; 111/1; 221/1
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A;Introns: 98/
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Parii, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
                                                                                                                                                                                                                                                        30-Sep-1989 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-475 <DEL3.
A; Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781
A; Note: this sequence was determined from the differentiated gene
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                       C; Accession: $01321
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immuno.
A; Reference number: $01320; MUID:88329081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 475;
58.9%; Score 1482.5; DB 2; Length
59.5%; Pred. No. 1.2e-77;
Live 69; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;20-475/Product: Ig gamma-2b chain #status predicted <WAT>F;159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-19/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision
                                                                                                                                                                                          gamma-2b chain precursor - mouse
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Query Match
                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                   homology
                                                                                                                                                                                                                                                                                                            Indels
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 < PAMI>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin 1
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                          Query Match 58.8%; Score 1481; DB 2; Best Local Similarity 60.0%; Pred. No. 1.5e-77; Matches 285; Conservative 66; Mismatches 112;
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PG4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp A;Reference number: JCS810; MUID:98063277
A;Rocession: PC4436
A;Molecule type: protein
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A; Residues: 1-444 <AKA>
C; Comment: This catalytic antibody has peroxidase oxidase activity. It
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <IMM>
F; 237-320/Domain: immunoglobulin homology <IMM>
F; 22/Disulfide bonds: interchain (to 98) #status predicted
F; 99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                                                                                                                                                                              :|| |::| ::|| |:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 SCDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
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                                                                                                                                                                                            5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMQWVRQAPGQ
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Length 374;
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Score 1443; DB 2;
Pred. No. 1.7e-75;
3; Mismatches 56;
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57.3%;
60.3%;
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Best Local Simil
Matches 267; C
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gamma 2b chain constant region - pig (fragment)
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R; Kacskovics, I.; Sun, J.; Butler, J.E.
R; Kacskovics, I.; Sun, J.; Butler, J.E.
R; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A; Reference number: 147159
A; Reference number: 147159
A; Accession: 147159
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                  230
196 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CP 253
                                                               254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
                                                                                288 PREEGENSTERSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYT 347
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A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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69.9%; Pred. No. 1.6e-65;
ive 42; Mismatches 52;
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CDNA sequences
Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C. Species: Sus scrofa domestica (domestic pig)
C. Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C. Accession: 147160
J. Immunol. 153, 3565-3573, 1994
A. Title: Five putative subclasses of swine IgG identified from the CDNA seq
A. Reference number: 147158; MUID: 95015845
A. Reference number: 147158; MUID: 95015845
A. Redesion: 147160
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Rolecule type: mRNA
A. Residues: 1-328 < KAC>
A. Residues: 1-328 < KAC>
A. Cross references: EMBL: U03780; NID: 9433125; PIDN: AAA52218.1; PID: 9433126
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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- protein search, using sw model OM protein

Run on:

August 14, 2002, 15:23:16; Search time 53.64 Seconds (without alignments) 339.265 Million cell updates/sec

US-09-499-662-157 2518 Perfect score: Title:

1 MGWSCIILFLVATATGVHSQ.........MHEALHNHYTQKSLSLSPGK 470 Sequence:

105224 segs, 38719550 residues Gapop 10.0 , Gapext 0.5

BLOSUM62DX

Scoring table:

Searched:

105224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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35	36 37 38	39 40 11	4 4 4 2 8 4	45

## ALIGNMENTS

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MEDLINE-71064024; PubMed=5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.; Waxdal M.J., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-82274238; PubMed-6287432;
Ellison J.W. Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
Nucleic Acids Res. 10:4071-4079(1982).
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SEQUENCE (MYELOWA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE OF 136-329 (EU).
MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-71064027; PubMed-4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin, X.
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SEQUENCE (MYELOMA PROTEIN NIE).
MEDLINE=77070269; PubMed=826475;
Ponstingl H., Hilschmann N.;
"The rule of a "The rule of 
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Last annotation update)
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SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
                                                          PRT;
                                                                                                               11-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequ
16-OCT-2001 (Rel. 40, Last anno
1g gamma-1 chain C region.
1GHG1.
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DISULFIDE BONDS.
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P01857;
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                                                                                                                                                          Delsenhofer J.;

"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-7 resolution.";

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"INSCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKER & THE GIM (NON-1) MARKER S.

"ISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

"MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                                     Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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R -> R (IN GIM(3) MARKER).
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D -> E (IN GIM(NON-1) MARKER).
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                                           MEDLINE-77070267; PubMed-1002129;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
Fram; PF00047; Ig; 3.
SWART; SM00410; IG_like; 1.
SWART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 2.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues 381-391 of human
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"Structural studies of immunoglobulin G.";
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MEDLINE-80114419; PubMed=118920;
Hofmann T., Parr D.M.;
A note of the amino acid sequence of
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"Characterization of the two unique
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                      SEQUENCE OF 2-326 FROM N.A.
MEDLINE=82197621; Pubmed=6804948;
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MEDLINE=84235992; PubMed=6329676;
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Mol. Immunol. 16:923-925(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%; Score 1610; DB 1;
91.8%; Pred. No. 1.9e-104;
tive 10; Mismatches 13;
                                                                                                                                                                                                                                                                                                       Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
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(Rel. 01, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                         CH3
                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW.
                                                                                         EMBL; J00230; AAB59393.1; -.
                                                                                                                                                                                                                           Pfam; PF00047; 19; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35884
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Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                         Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                         14
83
102
103
103
109
200
200
200
304
156
                                                                                                           PIR; A02148; G2HU.
HSSP; P01857; 1FC1.
MIM; 147110; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 AA;
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156
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220
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178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297
                      381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                 441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                            298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
                                                                                                                                 GC_RABIT
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        sednence of
                                                                                                       Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35940 MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                   SEQUENCE OF 1-30 AND 81-326.
MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.
"Human immunoglobulin subclasses. Partial amino acid constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1e-103;
  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 1599.5; 91.8%; Pred. No. 1e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                        EMBL; K01316; AAB59394.1; ALT_INIT.
                                                                                    SEQUENCE FROM N.A.
MEDLINE-83157104; PubMed-6299662;
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 3. SMART; SMO0410; IG_like; 1. SMART; SMO0407; IGcl; 2.
 OCT-2001 (Rel. 40, Last
gamma-4 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 303; Conservative
                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                           HSSP; P01842; 7FAB. MIM; 147130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 AA;
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                                                                                                                                                                                                                                                                                                                                   A02150; G4HU
                                                                 NCBI_TaxID=9606;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Blochem. J. 151:337-349(1975).
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                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.; "Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; "Heavy chain genes of rabbit 1961 isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                              323 AA.
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=76135469; PubMed=1243651; Pratt D.M., Mole L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed=6193512;
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MEDLINE=70110015; PubMed-5461106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-84030930; PubMed-6313520;
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                                                              STANDARD;
                                                                                                                                                                                                                                            Iq qamma chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
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                                                              GC_RABIT
P01870;
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Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                         pig
the (
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                                                                                                                                      Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunosjobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Mismatches
                                                                                                        SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=71058474; PubMed=4922544;
                                                                                                                                                                                                                                                                                                                          Biochemistry 13:4796-4803(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 13:4804-4811(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 3
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG; 2.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                       Biochemistry 10:9-17(1971).
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329 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Căvia porcellus (Guinea pig).
Bukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Euthoria: Rodentia; Hystricognathi; Caviidae; Cavia.
NCBL_raxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                         48.9%; Score 1231.5; DB 1; Length 323; 70.0%; Pred. No. 2.8e-78; Indels 7; Indels 7;
                                                                                                 M (IN D11 MARKER).

A (IN B15 MARKER).

E (IN REF. 2).

VPV (IN REF. 2).

E (IN REF. 5).

E (IN REF. 5).

E (IN REF. 5).

E (IN REF. 5).

O (IN REF. 5).
                                                                                                               1 -> M (IN ELE MARKER).

N -> E (IN REF. 2).

-> Vev (IN REF. 2).

-> D (IN REF. 5).

N -> D (IN REF. 5).

E -> Q (IN REF. 5).

E -> Q (IN REF. 5).

N -> D (IN REF. 5).

O (IN REF. 5).

N -> D (IN REF. 5).

N -> D (IN REF. 5).
                                                                   Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
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MEDLINE=71058471; PubMed=5538606;
                                                                                                                                                                     OZOZOHZHZ
                                                                                                                                                                                                                                                                                                                                                                           MW;
            Pram; PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE: PS00290; IG_MHC; 1.
IPR003597; Ig_c1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                    246
256
260
266
280
284
323 AA;
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                                                                                                                                    48
71
144
173
187
201
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P01862;
   InterPro;
                                                                                  NON_TER
VARIANT
CONFLICT
CONFL
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Best Local 9
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Biochemistry 10:26-31(1971).
-1- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN PIS: A02151; G2GP. Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."; carboxyl-terminal 140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199 Gaps SEQUENCE OF 227-311.

MEDILINE-75036073, Pubmed-4609467;

Trischmann T.M., Cebra J.J.;

"Primary structure of the CH3 homology region from guinea pig IgG2 SEQUENCE OF 134-226.

BEDLINE-7036072; PubMed-4429665;

Tracey D.E., Cebra J.J.;

"Primary structure of the CH2 homology region from guinea pig 1962 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTH--TCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 6 Score 1210.5; DB 1; Length 329; Pred. No. 8.1e-77; INTERCHAIN (WITH A HEAVY CHAIN). INTERCHAIN (WITH A HEAVY CHAIN). INTERCHAIN (WITH A HEAVY CHAIN). Immunoglobulin domain; Immunoglobulin C region; Glycoprotein INTERCHAIN (WITH A LIGHT CHAIN) 62; Indels 5D231B7164D1FBA9 CRC64

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-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
                                                      435
                           235
                                                                   MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL GATHE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.
MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM
318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene deletion model.";
Proc. Natl. Acad. G21. U.S.A. 79:3260-3264(1982).
-!- SUBBUNIT: DIMER LINKED BY 12 DISGLEIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISGLEIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HENYY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                    Frangione B., Rosenwasser E., Prelli F., Franklin E.C.; "Prinary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Blochemistry 19:4304-4308(1980).
              378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-7718561; Pubmed-402363;
Michaelsen T.E., Francione B., Franklin E.C.;
Primary structure of the 'hinge' region of human igg3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-77021516; PubMed-8233945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C., "The amino acid sequence of 'heavy chain disease' protein 20c. Structure of the fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3] REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC)
                                                                                                             469
                                                                                                                          296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
                                                                                                                                                                                                          290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
                                                                                                           436 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-81021548; PubMed-6774747;
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                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
                                                                                                                                                                                                        GC3_HUMAN
P01860;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Fittier are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      domain; Immunoglobulin C region; Glycoprotein; Repeat.
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DIMER).
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                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                           HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%; Score 1162; DB 1; 91.4%; Pred. No. 1.6e-73; ive 11; Mismatches 9;
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P -> L (IN OMM).
/FTId=VAR_003891.
F -> Y (IN OMM).
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC.
INTERCHAIN (WITH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> EB (IN ZUC)
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F -> Y (IN OMM).
/FTIG=VAR_003896.
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T -> A (IN OMM).
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                                                                                                                                                                                                                                                                                       HINGE.
CH2.
CH3.
                                                                                                                 EMBL; J00231; AAA52805.1; ALT_SEQ
                                                                                                                                                                     Interpro: IPR003006; Ig_MHC.
Interpro: IPR003597; Ig_c1.
Interpro: IPR003600; Ig_like.
Pfam; PF00047; ig; 2.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; IG_li I.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                               PIR; A02149; G3HUWI.
HSSP; P01857; 1FC1.
MIM; 147120; -.
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Best Local Similarity
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442
448
554
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                                                                     GCI_RAT STANDARD; PRT; 326 AA.
P20759;
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-1 chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                            "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
PIR; PS0017; PS0017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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013BAB45EF49B9DA CRC64;
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                419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                             region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%; Score 1155; DB 1; Length 326; 63.4%; Pred. No. 5.5e-73; tive 52; Mismatches 60; Indels 10
                          O
                                                                                                                                                                                                                                                                    PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                              CH1.
HINGE.
CH2.
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
Pfam; PF00047; 1g; 3.
SMART; SM00407; IGc1; 2.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-85027161; Pubmed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene."
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
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65.0%; Pred. No. 1.2e-72;
live 44; Mismatches 68;
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16-0CT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region, secreted form.
Mus musculus (Mouse)
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438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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CH2.
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PIR; B02156; G3MSC.
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01-AUG-1991 (Rel. 19, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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Best Local Similarity 65.09
Matches 215; Conservative
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380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
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MEDILNE-80012837, PubMed-113776;
MEDILNE-80012837, Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLIKRE-80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                SEQUENCE FROM N.A.

BEDILINE-BRO045036, Pubmed-115593;
HONJO T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                         GC1_MOUSE STANDARD; PRT; 324 AA. P01868; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 39-MAY-2000 (Rel. 39, Last annotation update) Ig gamma-1 chain C region. Mus musculus (Mouse).
                                                                        299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                       440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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J. Biol. Chem. 253:6068-6075(1978).
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MEDLINE-78242288; PubMed-98524;
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EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24175.1; -.
EMBL; V00793; CAA24175.1; -.
PIR; A02159; GIMS.
HSSP; P01842; 7FAB.
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Cell 18:559-568(1979).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Robrazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MGĎ; MGI:96446; Igh-4.
InterPro; IPR003096; Ig_MHC.
InterPro; IPR003997; Ig_cl.
Pfam; PF00047; ig; 3.
SWART; SMO477; IGcl. 2.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003600; Ig_like.
Pfan; SM00410; IG_like; 1.
SMART; SM00400; IG_like; 1.
PR0511F; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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Best Local Similarity 63.7
Matches 214; Conservative
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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ALERNATURE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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MEDLINE-82222190; PubMed-6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
                                                       .
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SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197625; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.
"mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
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                                                                                                                                                                                                              SEQUENCE OF 323-366 FROM N.A. MEDLINE-82115295; PubMed=6799207; Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl Eisenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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4CC88343B7A1CE27 CRC64;
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4. 79:2623-2627(1982).
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62.2%; Pred. No. 7.6e-72;
tive 55; Mismatches 60;
                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
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55; Mismatches
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Immunoglobulin domain; Immunoglobulin
Alternative splicing; Transmembrane.
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HINGE.
CH2.
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EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
PIR; B02129; GIMSM.
HSSP; P01842; 7FAB.
INTERPO: IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
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SMART; SM00407; IGc1; 2.
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393 AA;
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RESULT 13
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                                                                                                                                                                                             438
                  141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                           258
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                                                                                                                                  201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
                                                                                                                                                                                                                                                                                     319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-3 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-85027161; Pubmed-6092053;
Wels J.A. Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blather F.R.;
"Structural analysis of the murine 1963 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segment.";
Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, J00451; AAB59655.1; -.
EMBL, V01526; CAA24767.1; ALT_SEQ.
PIR, A02155; G3MSM.
HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003507; Ig_like.
Pfam; PF00047; ig_; 3
SMART; SM00410; IG_like, 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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P03987;
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MEDLINE=81198976; PubMed=6262729; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; "The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.", Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP--PCPAPELLG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178
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Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine
Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Sukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  4;
mmunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                          Length 398;
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                          45.2%; Score 1139; DB 1;
64.7%; Pred. No. 9.1e-72;
tive 44; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-2A chain C region, A allele.
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                                                                                                                                         POTENTIAL.
CYTOPLASMIC
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                                                                           HINGE.
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                                                            97
1113
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398 AA;
                                                                                                                                                                                                                                                                                                                               Similarity
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SEQUENCE FROM N.A.
                       Transmembrane;
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Matches 213;
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P01863;
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CONFLICT
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EEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438 

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               Ollo R., Auffray C., Morchamps C., Rougeon F.; "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.":
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                                                                                                                                                                                                                             MEDLINE=74175517; PubMed=4831970;
Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
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INTERCHAIN (WITH A HEAVY CHAIN).
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"Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Blochem. 30:452-462(1972).
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63.9%; Pred. No. 3.5e-71;
ive 43; Mismatches 73; Indels
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B84361C5445A6864 CRC64;
                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
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Immunoglobulin domain; Immunoglobulin C region.
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MEDLINE-81223894; PubMed-6787604;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_Like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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330 AA;
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                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                     MEDLINE-88166903; PubMed-312722;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemann co a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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66; Indels
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                                                                                                                                                         -FEB-1991 (Rel. 17, Last Sequence update)
-JUL-1999 (Rel. 38, Last annotation update)
gamma-2C chain C region.
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51; Mismatches
                                                                                                               329 AA
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439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
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HINGE.
CH2.
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InterPro; 1PR003006; 1g_MHC.
InterPro; 1PR003597; 1g_C1.
InterPro; IPR003600; 1g_like.
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SMART; SM00410; iG_like; 1.
SMART; SM00407; iGcl; 2.
PROSITE; PS00290; iG_MHC; 1.
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NON TER 1
DOMAIN 1 97
DOMAIN 98 113
DOMAIN 114 222
DOMAIN 223 329
DISULFID 15 15
DISULFID 27 82
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143
249
329 AA;
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Matches 209; Conserv
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HSSP; P0185
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                                                             377
                                                                          378 REEMIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                      318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82037777; PubMed-6794027;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Multiple amino acid substitutions between murine gamma 2a heavy chain Fc regions of igla and iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-82037861; PubMed-6170065;
Schreler P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
Schreler P.H., Bothwell A.L.M., Mueller-did sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                                                                                                                                                                                                                                           , Last sequence update), Last annotation update)
                                                                                                                                                                                                    438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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21-JUL-1986 (Rel. 01, Last sequence u
15-JUL-1999 (Rel. 38, Last annotation
IIG gamma-2A chain C region, B allele.
Mus musculus (Mouse).
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InterPro; IPR003006; 19_MHC.
InterPro; IPR003597; 19_C1.
InterPro; IPR003600; 19_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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HSSP; P01857; 1FC1.
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P01864;
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SEQUENCE
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Length 335;

Score 1126.5; DB 1; Pred. No. 5.3e-71;

44.7%; 61.6%;

Query Match Best Local Similarity

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                                     141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK-----SCDKTHTCPPCPA 254
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Gaps
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70;
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 Mismatches
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 52;
 Conservative
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Matches 207;
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August 14, 2002, 15:22:19; Search time 187.61 Seconds (without alignments) 433.386 Million cell updates/sec Run on:

US-09-499-662-157
2518
1 MGWSCIILFLVATATGVHSQ.....MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score:

Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Listing first 45 summaries

SPTREMBL\_19:\* Database :

sp\_archea:\*
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sp\_vortebrate:\* 44. 76. 110. 111. 113. 114. 116. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

SUMMARIES

	ID Description	1 Q9D8L4 mus musculu	1 Q99LC4 Mus musculu	099125 mus 1	099131 mus n	09r1a4			Q96PQ8 homo sapien		Овечае рошо	091wt3 mus	Q9BRV0 Q9brv0 homo sapien	omod 6dd960	Q91wt1 mus	Q96DK0 capien	
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Q9BU10 Q9BQB8 Q96AA6 Q99LA6 Q96K68	Q99KA4 Q91WP5 Q96EY0 Q91Z07	299M22 Q99M22 Q91X92 Q96KX8 Q9DPP6 Q9DCD9	Q91V67 Q9Y298 Q95978 Q924P9 Q96QS0	0924R3 0924D60 0924D5 0924P5 0924R8 0924R8
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764.5 760.5 754.5 753	738.5 735.5 731 714	669 667 643 591.5 586	523.5 523 520 508.5 508.5 495	494.5 482.5 479.5 477 477 473
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## ALIGNMENTS

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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00409; IG; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 K----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 IEKTISKPRGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 64.5%; Score 1623.5; DB 11; Length 473; al Similarity 62.8%; Pred. No. 1e-128; 299; Conservative 73; Mismatches 95; Indels 9;
                InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003509; Ig.
InterPro; IPR003006; Ig._like.
InterPro; IPR003006; Ig._NHC.
InterPro; IPR003596; Ig.v.
InterPro; IPR00409; Ig. 4.
InterPro; IPR00409; Ig. 2.
INTERPRO; IRRO, 1 IG. 2.
INTERPRO; IRRO, 1 IG. 3.
INTERPRO; IRRO, 1 IG. 1 IRRO, 1 IG. 3 IRRO, 1 IRRO, 1 IG. 3 IRRO, 1 IG. 3 IRRO, 3 I
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; ..
HSSP; P01842; 7FB.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003600; Ig.like.
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SIMILAR TO RIKEN CDNA 1810060009 GENE.
Bukaryota; Μετανία Μετανία Μουρου Μουρ
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Best Local Similarity
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099LC4;
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GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                   DB 11; Length 463
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888, AAH03888.1; -.
HSSP; P01842; 7FRB.
InterPro; IPR003599; Ig.
InterPro; IPR003609; Ig_cl.
InterPro; IPR003000; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 3.

SMART; SM00407; IGc1; 2.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                              64.0%; Score 1612.5; DB 1.62.7%; Pred. No. 8.2e-128; ive 75; Mismatches 90;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.7%,
Matches 296; Conservative
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96352328B3332ADB CRC64;

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51661 MW;
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437 AA;
                                                                                         Query Match
Best Local Similarity
   468 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                               Query Match 62.5%; Score 1572.5; DB 11; Length 473; Best Local Similarity 62.5%; Pred. No. 2e-124; Matches 297; Conservative 64; Mismatches 107; Indels 7;
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SMART; SM00406; IGV; 1.
SMART; SM004106; IG_11ike; 1.
PROSITE; PS00220; IG_MHC; UNKNOWN.1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
MUS MUSCUlus (Mouse)
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Q99L31
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[1]
SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scrv).",
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
HSSP: P01842; FRAB.
Interpro; IPR003606; Ig_like.
InterPro; IPR003066; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358
                                                                                                                                                                                                                                                 61 GOGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
                                           Gaps
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                                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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    Length 468;
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                                           Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
  ; Score 1550; DB 11;
; Pred. No. 1.6e-122;
63; Mismatches 109;
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_llke; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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61.6%;
62.3%;
                                             Matches 294; Conservative
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                                                                                                81 QKFKGRVTIITRDISISIAYMELSSLRSEDIAVYYCARNRDYSNNWYFDVWGEGILVTVSS 140
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                                                21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNYN 80
                                                               127 --FDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 184
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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     Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 57.0%; Score 1434.5; DB 11; Length 473; al Similarity 57.5%; Pred. No. 9.1e-113; 272; Conservative 73; Mismatches 113; Indels 15;
                           95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010327; AAH10327.1; -
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473 Aa; 51946 MW; CF625F008932AF12 CRC64;
  Score 1446.5; DB 11;
Pred. No. 7.9e-114;
); Mismatches 95; In
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091205;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                     439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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59.7%; Pre-
tive 70;
                            Conservative
             Similarity
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                        Matches 270;
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 Query Match
Best Local
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ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD 244
                                                                                                         298 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
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SEQUENCE FROM N.A.
MEDLINE-98383416; PubMed=9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant regic genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."
Immunobiology 199:105-119(1998).
EMBL: AJ30067; CAC44624.1;
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           358 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
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Matches 233;
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Q95M34;
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PPSREEMTKNQVSLICLVKGFYPSDIAVEWBSNGOP--ENNYKTIPPVLDSDGSFFLYSK 432
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
               240 APHPDELSKSKVSVTCLVKDFYPPEINIEWOSNGQPELETKYSTTQAQQDSDGSYFLYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                    MEDLINE=21477448; PubMed=11593034; MEDLINE=21477448; PubMed=11593034; Hu Z., Garen A.; Hu Z., Garen A.; Targeting tissue factor on tumor vascular endothelial cells an cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001). EMBL; AF272774; AAK58686.1; -. SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 701;
                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC012207; AAH12207.1; -
SEQUENCE 278 AA; 29778 WW; F894F955DDCD948A CRC64;
                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        ٥;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1257; DB 4;
Pred. No. 1.6e-97;
                                              433 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
|:||::|||| |:||||| 300 LSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK 337
                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                       701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.1%;
Matches 230; Conservative ;
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                               Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                    Q96PQ8
Q96PQ8;
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Q921K1
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                                                                                                                                                                          61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                            121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                      180 WNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSNNW--YFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 EKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD 357
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 614;
  Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN (PROTEIN FOR MGC:15420).
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.5%; Score 944.5; DB 4; Length 6 37.3%; Pred. No. 3.1e-71; Live 83; Mismatches 164; Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC009851; AAH09851.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TIEMBLIEL 19, Last sequence update) (TIEMBLIEL 19, Last annotation update)
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38.4%; Score 967; DB 11;
65.7%; Pred. No. 1.3e-73;
ive 35; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                    241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 37.3
Matches 215; Conservative
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                        Similarity
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01-DEC-2001
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                                            182;
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InterPro; IPR003599;
InterPro; IPR003597;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
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GK 463
                                            469 GK 470
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Matches 20
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                      358 QDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISE 415
                                                                                      375
                                                                                                                       SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP 475
                                                                                                                                                                        PSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY 430
                                                                                                                                                                                                                PAREOLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAH 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYIFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 DSSGYY---WGQGTTLIVSSEPAREPILYPLI-FPQALSSDPVIIGCLIHDYFPSGTMNV
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----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                    317 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.8%; Score 875.5; DB 11; Length 42.1%; Pred. No. 1.5e-65; Live 75; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488.1; -.
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                     431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                                                                                                                                                                                                                                                                                                                                   Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           Q91WT3 PRELIMINARY; PR. Q91WT3; Q91WT3; Q1-DEC-2001 (TrEMBLrel. 19, Crea O1-DEC-2001 (TrEMBLrel. 19, Last O1-DEC-2001 (TrEMBLrel. 19, Last HYPOTHETICAL 52.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.18
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-COLON;
                                                                                                                              416
                                                                                                                                                                        376
                                                                                                                                                                                                                476
                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNR- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK--------DTLM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYS---NNWYF---DVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPSQDVTV------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|| : | : | : | : | :|| | : | 343 WNHGKIFTCTAAAYPESKIPLATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARG
                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.4%; Score 866; DB 4; Length 500; 41.5%; Pred. No. 1e-64;
                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pram. PF00047; 19; 4.

SMART: SM00409; IG: 4.

SMART: SM00400; IG: 1.

SMART: SM00406; IG: 1.

SMART: SM00410; IG. 1.

SMART: SM00410; IG. 1.

Hyporhetical protein: SMRC; IG. MKNOWN_1.

SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
HOMO saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176;
                                                                                                                                                                                                                            Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67; Mismatches
                                                                                                                                                                                                                            500
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-PROSTATE;
Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005551; AAH05951.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1g.
1g_c1.
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                                                                                                                                                                                                                            PRELIMINARY;
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61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSSLGT-QTYICNVNHKPSNTKVDKRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 NCPGICSPPTTPPPPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 LIGTIAKVIVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 FWHYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 824.5; DB 11; Length
39.6%; Pred. No. 3e-61;
Live 76; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                  579
                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
481
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                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96DK0
Q96DK0;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 39.69
Matches 191; Conservative
                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=COLON;
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
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                                                                                                         Q91WT1
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                                                                       RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96DK0
ID Q9
AC Q9
DT 01
                                                                                          Q91WT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 PVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299
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                                       120 DYSNNWYF---DVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 SESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITFSWKIKNNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                  FYPSDIAVEWESNGO--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LSW----LFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARN-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPPSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 GSGVITDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCV
                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 119;
                                                                                                                                                                                                                                                                                                                                                             Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 N-----CDKTHTCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.8%; Score 826.5; DB 4; 33.0%; Pred. No. 2.8e-61; ive 93; Mismatches 178;
                                                                                                                                                                                                                597 AA
                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLE-1. 19, Crea 01-DEC-2001 (TrEMBLE-1. 19, Last 01-DEC-2001 (TrEMBLE-1. 19, Last HYPOTHETICAL 65.0 KDA PROTEIN. HOMO saplens (Human).

Eukaryota, Metazoa, Chordata; Cr Mammalia; Eutheria; Primates; C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------PCPAPELLGGPS-----
                                                                                      450 VMHEALHNHYTQKSLSLSPGK 470
                                                                                                           Submitted (OcT-2001) to the EM
EMBL, BC015760, AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.0°
Matches 192; Conservative
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                            RESULT 13
Q96BB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 1
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                  395
                                                                                                                        462
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16;
                                                                                                        386 ANLICTLIGL-RDASGVIFTWIPSSGK--SAVQGPPDRDLCGCYSVSSVLPGCAEPWNHG 342
                                                                                                                                                                                                                                                                                                                                                                            61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 VIVSWNSGALISGVHIFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPSNTKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK---------DTLMISRT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIAVEWESNGO--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHE 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVTV-------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLLLGSE
                                                                                                                                                                                                                                                                                                                                                                                                                              121 Y---SNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP-EP
                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN TRO
ALPHAI H,MYELOMA.
                                                                                                                                                                                                                                                                              Length 496;
                                                                                                                                                                                                                                                                            Ouery Match 32.2%; Score 812; DB 4; Length 49 Best Local Similarity 39.6%; Pred. No. 3.6e-60; Matches 197; Conservative 65; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALHNHYTQKSLSLSPGK 470
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completed: August 14, 2002, 15:22:21 ne: 689 sec Search com Job time: (